Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

50: gb_pl3:*

Page 1

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nu	nucleic search, using sw model
Run on:	March 18, 2000, 20:18:44; Search time 360.16 Seconds (without alignments) -3498.721 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-092-296-7_COPY_5_419 415 1 ACCGGACTICAGIGICICCAAAAITCGGIAIGCIGAAIT 415
Scoring table:	IDENTITY_NUC
Searched:	821193 segs, -1518192014 residues
Database :	GenEmbl: *
Word size :	0
Number of hits	that pass the threshold : 1642386 1: 90-bal:* 5: 90-pal:* 6: 90-ph:* 7: 90-ph:* 8: 90-pl:* 90

Score Match Length DB ID Description	Result NO. 1	33 34 14 25 25 25 25 25 25 25 25 25 25 25 25 25	S Query	re Lea	DB	-	Description
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37 32.4 7.8 184427 16 ENVV20824 U70824 Eguine 39 32.2 7.8 1822 2 AECONIS7 AECONIS7 AECONIS7 BOTZ 40 32.2 7.8 1212 3 PIGATA DIGATA AECONIS7 AECONIS7 AECONIS7 AECONIS7 AECONIST	m.	'n	œ.	2458	œ	AF052391	
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ALIGNMENTS

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Query Match 53.3%; Score 221; DB 11; Length 47323; Best Local Similarity 100.0%; Pred. No. 1.5e-55; Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps
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6285. 6572
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'Complement (8164...8609)

'Complement (1287...2895)

'Type (anily - Alu . 2295)

'Type (anily - Alu . 2295)
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complement(6972. .7050)
/rpt_family-*MLT1
7286. 7584
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/rpt_family-"MER20"
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ORIGIN
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This sequence Natidation:
This sequence has been validated by Multiple Complete Digest
Mapping, Comparison of the experimentally derived map digest
fragments with sequence-predicted tengents is given below
small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.
Hindill
Map
Seq
Map
Geraghty, D.E.
Large scale sequence analysis of the human MHC class I region
Large scale sequence analysis of the human MHC class I region
Large scale sequence analysis of the human MHC class I region
Large scale (1989)
Fred Hutchinson Cancer Research Center
The Clinical Research Division
Life Chinical Research Division
Life Chinical Research Division
Scattle, WA 98109-1024
E 2 (bases I to 47323)
S Direct Submission
L Submitted (05-WV-1998) Human Genome Center, University of Mashington, Box 35145, Seattle, WA 98195, USA
University of Washington Human Genome Center
Box 35145 Seattle, WA 98195
Contact: Daniel E: Geraghty (geraghty@fhcrc.org)
Overlapping Sequences:
S: UMGC:170m23.013 (Genbank Accession: AC00530)
3:: UMGC:y67cll12 (Genbank Accession: AC004211)
                                                                                                                                                                                                                                                                                                                                                              Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
a rico in 10,000 pp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ass. If ile.
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/sub_cione="UWGC.370M23.002"
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1. .47323
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Direct Submission
Submitted (1-SEP-1999) to the DDBJ/EMEL/GenBank databases. Mika
Hirakawa, Japan Science and Technology Corporation (JST), Advanced
Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
Japan (E-mailimika@tokyo.jst.go.jp,
WELihttp://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japan Science and Technology Corporation (JST)
5-3 Yonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan
For further infomation about this sequences, please visit our
sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.
html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
Location/Qualifiers
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/note="CdaOvhlO;The location is between each flanking site of Forg primers."
/db.xref="GDB:443382"
142030. .142159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is conducted by Tokai University as a JST sequencing
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/standard_name="D6S2088"
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                                                                                                                                                                                                                                                                                                                                                      1 (sites)
Shidna, S., Tamiya, G., Oka, A. and Inoko, H.
Homo sapiens 2, 229, 818bp genomic DNA of 6p21.3 HLA class I region
Published Only in DateBase (1999) In press
2 (bases 1 to 200000)
Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     flanking site
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Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
section 10/20.
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/note="SHGC-16870;The location is between each flanking
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complement(142479. 142740)
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site of PCR primers."
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Eutheria; Primates; Catarrhini, Hominidae, Homo.
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Phone: H81-463-93-1121, Fax: +81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALIS
project of JST
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/note="RH18132;The location is between each
of PCR primers."
  Db 178381 CCCICCTGAGCGCAATAAAATACGGTATGCTGAATT 178421
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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AP000511.1 GI:5926698
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Shidna,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
Katanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahram,S. and Inoko,H.
Molecular dynamics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp HLA class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Totals 1 to 192650)
Shina.T. and Takishima.N.
Direct Submission
Submitted (29-JaN-1999) to the DDBJ/ENBL/GenBank databases. Takashi Shina. Tokai University School of Medicine, Department of Molecular Life Science 2; Bohseidal, Isehara, Ranagawa 259-1193, Japan (E-mail:tshina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
05 178261 CICAACACCAIGITGICIGCAACACATGAAGCCATGAAGCCTGTGTGCCTTTTGGCCC 178320
                                                                                                              AB023048 192650 bp DNA PRI 20-NOV-1999 Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region, close:5319, complete sequence.
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                                                                                                         374
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Eutheria, Primates; Catarrhini, Hominidae, Homo.
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                                                                                                                                                                       saplens cell_line:978SK ONA, clone:53L9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saptens
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Center code: BCM who, become the content code attent bayon Content code: http://www.hgsc.bcm.tmc.edu/
Contentci hgsc.hclp@bcm.tmc.edu
Content; hgsc.hclp@bcm.tmc.edu
Content; pgve-terminator Big Dye: 100% of reads
Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.980611
Consensus quality: 180910 bases at least Q40
Consensus quality: 180920 bases at least Q30
Consensus quality: 181852 bases at least Q30
Consensus quality: 181852 bases at least Q30
Consensus quality: 181852 bases; sum-of-contigs estimation
Estimated insert size: 182066; sum-of-contigs estimation
Quality coverage: 5.1x in Q20 bases; sum-of-contigs estimation
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Submitted (SacOr-1999) Human Genome Sequencing Center, Department
Submitted (SacOr-1999) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 10, 1999 this sequence version replaced gi:6325499.
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                 ACO12467 185548 bp DNA HTG 09-DEC-1999 HOMO SAPIENS CLONE RP11-884K10, *** SEQUENCING IN PRQGRESS ***, 8 unordered pieces.
                                                                                                                                                  244 CCAIGCAAGAICICAACACCAIGIIGICIGCAACACACAIGACAGCCAIIGAAGCCIGIGIC 303
                                                                                                                           304 CITCIIGGCCCGGGCITIIGGGCCGGGGAIGCAGGAGGCAGGCCCCGACCCTGICIIICA 363
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                                                                                                                                                                                                          364 GCAGGCCCCCACCTCCTGAGTGGCAA 390
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Worley, K.C.
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HTG; HTGS_PHASE1.
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                    complement(14525. 164665)
/note="SHGC-3064/The location is between each flanking site of PCR primers."
/db_xref="EGDB:1234116"
complement(169209. 169574)
/standard_name="D68952"
/note="Trigon" is between each flanking site of PCR primers."
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DD 110528 AGCICIGCCTCCTCCATCTCCCTTCAGGGACCAGGGTCACCATCCACCATGCAAGAI 110587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 ATTGCTTGAAAAGCTCTGCCTCCTCCTCCCTTCAGGGACCAGCGTCACCTCCA 243
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52.9%; Score 219.4; DB 10; Length 200000;
Best Local Similarity 99.5%; Pred. No. 5e-55;
Matches 220; Conservative 0; Mismatches 1; Indels 0; G
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10.2%; Score 42.2; DB 5; Length 7218;
Best Local Similarity 2.8%; Pred. No. 0.033;
Matches 11; Conservative 214; Mismatches 162; Indels 0
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Unclassified.
1 (bases 1 to 7218)
2 Dorner, F., Scheifilinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Recombinant townpox virus
Patent: US 5570367-8 14 23-SEP-1997;
Location/Qualifiers
1. 7218
1. 7218
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1491 c 1486 g 1929 t
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52605 a 47531 c 49366 g 50498 t
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Sequence 14 from patent US 5670367.
166494.1 GI:2724471
            'db_xref="GDB:675281"
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Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (Dases 1 to 118276)

Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Barnes, N., Beckerly, R., Benn, J., Colling, S., Collymore, A., Cocke, P., Colngis, D., Depayre, E., Forrest, C., Funk, R., Colngha, D., Cocke, P., Colligs, D., Depayre, E., Forrest, C., Funk, R., Collymore, P., Collymore, E., Forrest, C., Funk, R., Collymore, D., Gardigey, K., Grant, G., Jacottch, L., Jones, C., Kann, L., Horton, L., Honland, J.C., Jacottch, L., Jones, C., Kann, L., Martian, M., Morris, M., Morrow, J., Mychalecky, J., Macdonald, P., Marquis, N., McDents, R., Mychalecky, J., Malla, M., Morris, M., Morrow, J., Mychalecky, J., Stanger Thomann, N., Stilvell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella Willer, I., Vo, A., Magner, A., Wheeler, J., Wu, Y., Wyman, D., Vasaillev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Direct Submission and Zody, M. (and 28, 1998 this sequence version replaced gi:3402743.

Green, P. (1996-1997)

Ince (1981-1997)

Ince (2016-1997)

Ince (2016-1997)

Ince (2016-1997)

Ince (2016-1997)

Ince (2016-1997)

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complement(1975. .2142)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 100605 TCTCTTCTCATTATATATGTCTCTGGGAGGAAAACACTTGTTAGAAGCTGTATCT 100548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 GCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 AITGCTIGAAAAGCTCTGCCTCCTCCATCTCCCTTCAGGGACCAGGGTCACCTCCA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 CCITGICCICCICITGACCCICCTIGGCAGCICACAIGGAACAGGGCCGGGIAIGACIIT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC004148 118276 bp DNA PRI 28-AUG-1998
Homo sapiens chromosome 17, clone HCIT524C5, complete sequence.
AC004148
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 11876)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone HCIT524C5
Unpublished
2 (bases 1 to 118276)
Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 CCATGCAAGAICTCCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTGTGTC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.0%; Score 37.2; DB 45; Length 185548; Best Local Similarity 45.3%; Pred. No. 1.3; Matches 135; Conservative 0; Mismatches 163; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 CITCITGGCCCGGGCITTIGGGCCGGGGAIGCAGGCAGGCCCCGACCCTGTCTT 361
consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as tuns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                      372 others
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complement (2301 . 23466)

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Butheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 65870)

1 (bases 1 to 65870)

Evans, G.A., Athanasiou, M., Aguayo, P., Armstrong, D., Basit, M., Buettner, J., Bumelster, R., Card, P., Gesalboat, F., Dunn, J., English, C., Ethridge, S., Garner, H.R., Gee, V., Gordon, M., Gotway, G., Grant, O., Hahner, L., Josiln, J., Lewis, E., Loo, H., Loo, K. N., Major, T., McFarland, J., Newton, J., Oobbrne-Lawrence, S., Schageman, J., Schultz, R.A., Stimson, S., Syed, M. and Ward, T. HTGS Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD 68751 GAIGATGTACTGTCATATAAATCCACTAAATCCAGCAACAAGAACTGCCTGG 68692
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Mus musculus Chromosome 17 BAC clone citb585c7 from MHC region,
complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 GCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTGGAATTGCTTGA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD 68691 AACTGTGGCCATGTTTTTTTTTTTTTAAGACCAGTGTGATAGTAGGCCATGCA 68634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 AAAGCICICCICCICCICCAICTCCCIICAGGGACCAGCGICACCCICCACCAIGCA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
8.8%; Score 36.4; DB 11; Length 118276;
Best Local Similarity 56.8%; Pred. No. 2.2;
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Euthoria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

1 (Assa 1 to 207092)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP11-321F6

Oppublished

2 (Assas 1 to 207092)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balren, B., Linton, L., Beckerly, R., Boguslavkly, L., Boukhgalter, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A HTG 03-DEC-1999 clone RP11-321F6 map 15, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5064 TGGAGCAGAGCTGGCGGGATTTTGGCAGCCCCTCTAGGAGAAATGTTTTGGGAAAGACTC 5005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 CTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 ITCAGGGACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGGAACAC 279
                          consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                   s: contig of 2666 bp in length
s: gap of unknown length
s: contig of 5451 bp in length
s: gap of unknown length
s: contig of 6266 bp in length
s: contig of 10968 bp in length
s: contig of 10968 bp in length
s: gap of unknown length
s: contig of 10321 bp in length
s: contig of 2088 bp in length
s: gap of unknown length
s: contig of 22084 bp in length
s: contig of 22084 bp in length
s: contig of 52021 bp in length
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53798 a 51576 c 52041 g 50425 t
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Best Local Similarity 49.7%; Pred. No. 4.5;
Matches 90; Conservative 0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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SEQUENCE, 19 unordered pieces.
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Unpublished

Ye Chases 1 to 68870)

Evans,G.A., Athanaslou,M., Aguayo,P., Armstrong,D., Basit,M.,
Buettner,J., Butler,C., Card,P., deSallboat,C., Dunn,J.,
English,C., Ethridge,S., Garner,H.R., Gordon,M., Grant,O.,
Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N., Major,T.,
Schillz,R.A., Stimson,S., Wagner,N., Waller,K. and Ward,T.
Direct Submission
Submitted (10-0CT-1998) Genome Science & Technology Center,
University of Texas Southwestern Medical Center, 5323 Harry Hines
Blvd, Dallas, IX 7523-8891, USA
3 (bases 1 to 65870)

Svans,G.A., Athanaslou,M., Aguayo,P., Armstrong,D., Basit,M.,
English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
Schageman,J., Schultz,R.A., Slimson,S., Waller,K. and Ward,T.
Direct Submission

L. Schageman,J., Schultz,R.A., Slimson,S., Waller,K. and Ward,T.
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ON Mar 13, 1999 this sequence version replaced gi:4138779.
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-DEC-1998) Genome Science & Technology Center, University of Texas Southwestern Medical Center, 5323 Harry Hines Blvd, Dallas, TX 75235-8591, USA
On Dec 1, 1998 this sequence version replaced gi:3738098.
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Homo sapiens clone NH0132A01, *** SEQUENCING IN PROGRESS ***,
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Eutheria Frimates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 207984)
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llarity 50.3%; Pred. No. 2.4;
Conservative 0; Mismatches 88:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
db_xref="taxon:10090"
15739 c 14910 g 18197 t
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Gaps

TITLE JOURNAL COMMENT

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Direct Submission Submitted (17-OCT-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, NG MO 63108, USA On Oct 22, 1999 this sequence version replaced 91:6065437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 118979 CCCCCTAGCCCCTGGAGGTTGTTCAGGCCTCAAGCCAGGCCAGCCTGAAGATTCCTTATTC 119038
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Homo aspiens chromosome unknown clone NH0163G21, WORKING DRAFT
SEQUENCE, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 AAAGCTCTCCTCCTCCTTCCCTTCAGGGACCAGCGTCACCTCCACCATGCAAG 252
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1 (bases 1 to 148231)

2 (slaston, J.E. and Waterston, R. -

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)
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The sequence of Homo sapiens unknown clone NH0163G21
Unpublished
3 (bases 1 to 148231)
104530: contig of 11615 bp in length gap of unknown length 116338: contig of 11808 bp in length gap of unknown length gap of unknown length 150924: contig of 12124 bp in length gap of unknown length 179884: contig of 2462 bp in length gap of unknown length 179884: contig of 28960 bp in length 207092: contig of 27208 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_"RP11-321F6"
/clone_11b="RPCI-11 Human Male BAC"
52024 a 50991 c 51948 g 52004 t 125 others
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                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. 207092
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
/map="15"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Department of Genetics
Washington University
St. Louis MO 63108, USA
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TITLE
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     Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArcellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreitar, P., Fitzhudh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Crant, G., Funke, R., Gage, D., Galagan, J., Gardyna, S., Crant, G., Hagos, B., Heaford, A., Morton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McGenan, K., McLaughlih, J., Marquis, N., McDwan, P., McGurk, A., Wardonald, P., Marquis, N., Peterson, K., Pollara, V., Rilby, R., McYan, Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teafaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M. Noll, Usa Direct Submission

AL Submitsed (13-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 0214, USA

On Dec 3, 1999 this sequence version replaced 91:6403701.

All repeats were identified using Repeathasker. html

Center whitehead Institute/ MIT Center for Genome Research

Center of Genome Center

Center in Whitehead Institute/ MIT center for Genome Research

Center project information

Center project information

Center project name: 12382

Center close name: 12382

Center project name: 12382

Consensus quality: 196756 bases at least Q20

Consensus quality: 197001; squrose-fp

Insert size: 197000; squrose-fp

Insert size: 197000; squrose-fp

Guality coverage: 5. 3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1964: contig of 1964 bp in length
4257: contig of 2293 bp in length
4257: contig of 2293 bp in length
gap of unknown length
11026: contig of 4492 bp in length
gap of unknown length
14793: contig of 2277 bp in length
gap of unknown length
21436: contig of 3767 bp in length
gap of unknown length
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40070. .40288
42643. .40288
47624. .40127
44800. .4117
70tc="pseudogene similar to PID:g1070603 collagen alpha
1(III) chain precursor - human"
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21415. 218%
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family="MER21-group"
1. .34593
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85966. 36099
rpt_family="MIR"
86605. 36841
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/ypt_family="Malk"
/49866..50010
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32576. 32706
/rpt_family="MIR"
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.47571
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4594. .35003
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51046. .51183
/rpt_family="L2"
51453. .51806
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9216. .49583
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1807. .52111
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52112. .52185
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6918. .47149
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46140. .46559
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17503. .47
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                                                            NOTICE: This 'working draft' quality sequence may consist of several contigs from automated sequence assembly concatenated together. No attempt has been made to order or orient the contigs relative to one another correctly before concatenating. At each location in the sequence where contigs have been joined, several consecutive Ns may have been inserted.
                                                                                                                                                                                                                             The attached annotation was produced using a purely automated
                                                                                                                                                                                                                                                                                              The location of this clone is unknown.
* NOTE: This is a "working draft" sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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16750. 16798
/rpt_family"(TA)n"

    148231
    organism="Homo sapiens"
/db_xref="taxon:9606"

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20606. .20663
/rpt_family="Retroviral"
20665. .20723
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5774. .5951

**Pt_family="(TGAG)n"

3803. .8851

**Pt_family="MIR"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_limbunkown"
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196. 2601
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2720. .13002
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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of 1096 bp in length
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of 1145 bp in length
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of 2057 bp in length
unknown length
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of 1363 bp in length
unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC012184 65673 bp DNA HTG 21-OCT-1999
Homo sapiens chromosome 16 clone RPCI-11_529K1, *** SEQUENCING IN
PROGRESS ***, 40 unordered pleces.
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1 (bases 1 to 65673)

DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
Unpublished
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 148231;
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                                                                                                                                                                                                                                                                                                                                                                                           7034. .57065
rpt_family="AT_rich"
7430. .57728
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54419. .54720
/rpt_family="Alu"
54721 .54803
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DOE Joint Genome Institute.
                                                                                             /rpt_family="Malk"
54110. .54357
/rpt_family="Alu"
54358. .54418
                   /rpt_family="Malk"
52475. .52955
/rpt_family="L2"
53870. .54109
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55944. .56399
/rpt_family="MaLR"
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/rpt_family-"L1"
55769. .55940
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AC012184.1 GI:6091684
HTG; HTGS_PHASE1.
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on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl RP1-144C9 is from the library RPC1-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.3%; Score 34.4; DB 10; Length 77322; 63.1%; Pred. No. 8.4; Live 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                  This sequence is the entire insert of clone RP1-144C9 Location/Qualifiers
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Mus sp. DNA for oxytocin receptor, partial cds.
D86631
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/note="match: GSS: Em:A0627537.1"

complement(11439. .11580)

/note="match: GSS: Em:A0307187"

complement(24560. .25030)

/note="match: GSS: Em:A0307331"
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/hote="match: GSS: Em:AQ114724"
47849. .48201
/hote="match: GSS: Em:AQ553574.1"
63243. .63496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1710. .2227)
//note="match: 6SS: Em:AQ355665"
complement(1780. .2227)
/note="match: GSS: Em:AQ355618"
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27999. .28360
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29391. 29649
/note="match: STS: Em:G06203"
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Mus sp. (strain:1295V) ES cell DNA.
Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Homo sapiens"
/db_xref-"taxon:9606"
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/clone="RP1-144C9"
/clone_lib="RPCI-1"
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D86631/c
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Submitted (22-W1919) Sanger Centre, Hinxton, Cambridgeshire, Clan Clan Carlon State of Submitted (22-W1919) Sanger Centre, Hinxton, Cambridgeshire, Clan Carlo Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; IT:, TREMBL; Wp:, WORMDEP; Information ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSDJ144C9 77322 bp DNA PRI 22-NOV-1999
Human DNA sequence from clone RP1-144C9 on chromosome lp34.3-36.11,
complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 39815 IGAAAAACICTCCATCCACCCCTCCGTCTCCGGACGGGGGGCCCCCTGACCCCTTC 39756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 TGAAAAGCICIGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCAIGC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 AAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTGTGTCCTTCTT 309
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 77322)
Hall, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 8.3%; Score 34.6; DB 42; Length 65673; Local Similarity 54.3%; Pred. No. 7.2; hes 70; Conservative 0; Mismatches 59; Indels 0;
9ap of unknown length
1525 53246: contig of 4502 bp in length
9ap of unknown length
9ap of unknown length
9247 56192: contig of 1722 bp in length
9ap of unknown length
6193 58896: contig of 2946 bp in length
9ap of unknown length
9ap of unknown length
9ap of unknown length
9ap of unknown length
1546: contig of 2704 bp in length
9ap of unknown length
1547 65673: contig of 2650 bp in length
15573 contig of 4127 bp in length
1. 65673

/Organism="Homo sapiens"
/Obranosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 others
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16632 c 16336 g 15686 t
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/chromosome='22"
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/clone="RP5-85816"
/clone="RP5-85816"
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/style
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/product="dJ858B16.1.1 (KIAA0542 (isoform 1))"
join(<273. 454.1413. 1488.1978. 2073,2338. 2614,
join(<373. 454.1413. 1488.1978. 2973,2338. 2659,10811. 10885,
31023. 11199,11271. 12948.14414. 14546,14669. 14747,
15784. 15895,15983. 16218)
                                                                                                                                                                                                                        Submitted (25-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire, Submitted (25-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. F.-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Jul 27, 1999 this sequence version replaced q1:5579004.
Outling sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variationa where differences are found these are annotated as variational rogether with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with conty a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databasea: numbers given in the feature table with their source databasea: Ems.; EmBL; Sw., SMISSPROT; Tr., TREMEL; Wp., WORMPEP; Information on the WORMPEP database can be found at his hear finished according to sequence map criteria as follows. An attempt is made to resolve all sequencement problems, such as compressions and repeats but not necessarily within known compressions and repeats equence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 human chromosome 22, constructed by the Sanger Centre Chromosome 22 http://www.sanger.ac.uk/HGP/Chr22

http://www.sanger.ac.uk/HGP/Chr22

Cancer Institute by the group of pieter de Jong. For further Cancer Institute by the group of pieter de Jong. For further Cancer Institute by the group of pieter de Jong. For further Cancer Institute by the group of pieter de Jong. For further INF sequence is not the entire insert of clone 858B16. It may be shorter because we only sequence overlapping aections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone 694E4 (AL031255) is at 36572 in thia
                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; primates; Catarrhini; Hominidae; Homo.
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1. .36676
/organism="Homo sapiens"
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Barlow, K.
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// LEGALSONAL ANGERPANNSIELDLGSCUPPGAEGNLIAGPPRNEALARVEVA
// LEGALSONACVLLALRTRHKHSRLFFRKKLSIADLVVAYFOVLFOLLMOIT
RRFYGPDLLCRLVKYLOVVGMFASTYLLLLMSLDRCLATCOPLRSLRRFIDRLAVIAT
WLGCLLASYPOYHIESELREVACYPDCRAYFTQPNGPRAYTYTHILAVYIVPVIVLA
WLGCLLASYPOYHIESELREVACHTORANDANASCGAGRAALARVSVKLISKAKIRIVVKM
FIIVLAFIVCWTPFFFVQMMSVWDVNAPKE"
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Kubota, Osaka University Medical School, Department of Obstetrics and Gynecology; 2-2 Yamadaoka, Suita, Osaka 565, Japan (E-mail:kubota@gyne.med.osaka-u.ac.jp, Tel:81-6-879-3351, Fax:81-6-879-3359)
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                                                                                                                                                               (bases I to 3626) (Kubota, Y., Kimura, T., Hashimoto, K., Tokugawa, Y., Kimura, T., Azuma, C., Saji, F. and Murata, Y. Structure and Expression of the Mouse Oxytocin Receptor Gene
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/protein_id="BAA18996.1"
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/cell_type="ES cell"
1. 1530
1531. 1798
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/number=1
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/number=2
2394. .2485
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2486. .3547
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// Ugette—" Gao Sablo.
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19003. .19141,19318. .19554,21353. .21518,23432. .23685,
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                              Db 14428 GGCTACTCCTAGGGATAAGCCCCCCGGTCCTCATCCTGGCCAGTGTCCCTGACCCCCA 14487
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/note="LTR40a repeat: matches 1. .100 of consensus"
7929. .8097
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14669. .14747,15784. .15895,15983. .16087,
70sne="40458816.1"

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FGENES and GENSCAN*
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Kkafclwresaqglrtertgrvraaefhmaqllrmawsqmreclalrgaerqklmrad
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            /note-"match: CNNAs: Em:AB011114"
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/db_xref-"G1:5921489"
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* 11207 12024; contig of 818 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 816 bp in length gap of unknown length contig of 803 bp in length gap of unknown length	19233: contig 20042: gap of 20856: contig 20856: contig 20857: contig 24657: contig 24065: contig 24065: contig 24065: contig 24065: contig 24065: contig 24075: contig 26475: contig 26475: contig 26475: contig 28075: contig 28076: contig 28076: contig 28076: contig 28077: contig 28076: contig 28077: contig 28076: contig 28077: contig 28077: contig 28077: contig 28071: contig 32021: contig	
Eutherla; Primates; Catarrhini; Hominidae; Homo. REFERENCE I (bases 1 to 62181) Birren, B., Linton, L., Nusbaum, C. and Lander, E. JOURNAL Homo Sapiens, clone RPI1-655M17 JOURNAL Unpublished 2 (bases 1 to 62181) Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Brown, A., Castlel, M., Collins, S., Collymore, A., Cooke, P., Dearellano, N., Beckerly, R., Boguslawkiy, L., Boukhgalter, B., Refereira, P., Fitzkugh, M., Collins, S., Collymore, A., Cooke, P., Dearellano, W., Domino, M., Donelan, L., Doyle, M., Conke, P., Doneson, C., Tonkon, S., Gardy, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Joneson, C., Rusk, P., Maratas, A., Klein, J., Horbon, J., Horbon, L., McEwan, P., McGurk, A., McKennan, K., McMaughin, J., McEwan, P., McGurk, A., McKennan, K., McLaughilin, J., Meldrim, J., McTowy, J., Naylor, J., Naylor, W., Stiley, R., Sautos, K., Sevey, P., Centano, M., Palamas, J., Chandan, R., Pollara, V., Riley, R., Sautos, K., Sevey, R., Sevey, P., Chandy, R., Pollara, V., Riley, R., Soy, A., Talamas, J., Ralands, J., Ralands, J., Talamas, J., Tal	Wyman, D., fe, W.J., inner, A. and Zody, M. Direct Submission JODRNAL Submitted (24-09-1999) Whitehead Institute/MIT Center for Genome Submitted (24-09-1999) Whitehead Institute/MIT Center for Genome All repeats were identified using RepeatMasker: All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) Center code: WIBR Genter code: Wills Was site: http://www.seq.wi.mit.edu Contact: sequence submission@ence.wi.mit.edu Contact: sequence submission@ence.wi.mit.edu Contact: sequence submission@ence.wi.mit.edu Contact: sequence submission@ence.wi.mit.edu Scottigo: Russ of Nate used to separate the reads ** and the order in which they appear is compleacly ** and the order in which they appear to be deduced. ** However, it should not be assumed that this clone ** the record is updated, the accession number will ** be preserved. ** 775 1589 contig of 808 bp in length ** 1372 3186 3980 contig of 775 bp in length ** 3981 4778: contig of 785 bp in length ** 3981 4778: contig of 808 bp in length ** 3981 4778: contig of 808 bp in length ** 3981 4778: contig of 808 bp in length ** 3981 4778: contig of 808 bp in length ** 3981 4778: contig of 808 bp in length ** 3981 4778: contig of 808 bp in length ** 3981 4778: contig of 808 bp in length ** 3981 4778: contig of 808 bp in length	5584: Cont.19 929 0 6392: Cont.19 929 0 7189: Cont.10 929 0 8802: Cont.10 9603: Cont.10 929 0 920 0 11206: Cont.11206: Cont.11

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40741: contig of 731 bp in length gap of unknown length 41570: contig of 829 bp in length 42298: contig of 728 bp in length gap of unknown length 62298: contig of 682 bp in length gap of unknown length 63786: contig of 682 bp in length gap of unknown length 64532: contig of 808 bp in length gap of unknown length
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Ouery Match 8.1%; Score 33.8; DB 44; Length 62181; Best Local Similarity 53.4%; Pred. No. 12; Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Oy 126 AACTGAAGCTGAA 138

Search completed: March 18, 2000, 20:24:08 Job time: 1518 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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March 20, 2000, 09:31:54 ; Search time 76.27 Seconds
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Title: Perfect score: Sequence:

US-09-092-296-7_COPY_5_419 415 1 ACCGGGATTCAGTGTCTCC......AAAATICGGTATGCTGAATT 415

Scoring table: IDENTITY_NUC

311585 seqs, 125096042 residues Searched:

N_Geneseq_36:* Word size : Database :

623170 Number of hits that pass the threshold : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2262 5018 5018 5018 5350 325	cDNA to mRNA; 439 rst entry) otein; HP10408; hu Location/Qualifier. 75. 311 /*tag= a /note= "cDNA compr. 445. HEW RES CENTRE. 4. Tamaguchl T; 4. Tamaguchl T; 6. The stop of region of sell production, gell region of sell production, gell production of also chain (see W88498) DNA library using trotein (see W88498) DNA library using the region of as compositions stream of containing the vectors containing the vector as compositions stream of production of	89 89 89 100 100 tive	51-15 1-15 1-15	CTTG2 CTTG2 CTTG2 SAAG6
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Matches 53; Conservative
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This sequence represents a nucleic acid molecule which encodes a secreted
                                                                                                                                                                                                                                     Human secreted protein gene 16 clone HSHBQ68.

Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; itssue; cancer; tumour; neurodegenerative disorder; leukaemia;
developmental bunormality; foetal deficiency; blood; allergy; renal; dis-
inflammetion; ischeemic shock; Alzheimer's disease; brain; hepatic; lymphoma;
inflammetion; ischeemic shock; Alzheimer's disease; restencials; AIDS;
cognitive disorder; schlzophrenia; prostate; obesity; osteoclast; thymus;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                            CCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTGT 300
                                                                             389 TCAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG 439
                                                                                                                           361 TCAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATTTCGGTATGCTG 411
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Y, Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM,
Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi
                                                                                                                                                                                                        X04326 standard; DNA; 2923 BP.
                                                                                                                                                                                                                              13-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1998 U12125.
13-JUN-1997 US-061066.
13-JUN-1997 US-061066.
13-JUN-1997 US-049549.
13-JUN-1997 US-049549.
13-JUN-1997 US-049560.
13-JUN-1997 US-049608.
13-JUN-1997 US-049608.
13-JUN-1997 US-049609.
13-JUN-1997 US-049609.
13-JUN-1997 US-049609.
13-JUN-1997 US-049611.
13-JUN-1997 US-049611.
13-JUN-1997 US-059866.
13-JUN-1997 US-059866.
13-JUN-1997 US-058669.
12-SEP-1997 US-058669.
12-SEP-1997 US-058669.
12-SEP-1997 US-058869.
12-SEP-1997 US-058868.
12-SEP-1997 US-058868.
12-SEP-1997 US-058868.
12-SEP-1997 US-058875.
12-SEP-1997 US-058875.
12-SEP-1997 US-068844.
02-0CT-1997 US-060844.
02-0CT-1997 US-060844.
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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from base 300001 (Borrella burgdorfer1 polynucleotid
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human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. X04302) for increasing the stability of the fused protein as compexed to the human protein only.

The invention relates to 86 novel genes and their fragments (nucleic acid sequences: X04311-x04410; amino acid sequences W78126-W78225) which are useful for preventing, treating or ameliorating medical conditions es. 9. by protein or gene therapy. Also, pathological conditions on be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynelocides. Specific uses are described for each of the 86 polynucleotides, based on which tissues they are most highly expressed in (see X04311 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  v28846;
3.AUG-1998 (first entry)
Mouse coxsacklevirus and adenovirus receptor encoding DNA.
Mouse; coxsacklevirus; adenovirus; receptor; CAR; cardiac Infection;
myocarditis; pericarditis; dilated cardiomyopathy; meningoencephalitis;
panoreatic infection; acute panoreatitis; gastrointestinal tract;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41203 AAGCTCTGCAAGCTCTGAAGCAGCAATCTCTTCATCCTCACCTCAGCACATATCAAAAG 41262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 TCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 CICCICCICCAICICCTICAGGGACCAGCGICACCTICCACCAIGCAAGAICICAACAC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 TGTCTCCTCCATCCCAGGAGGGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 110000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 34.4; DB 1; Length 2923; 63.1%; Pred. No. 0.47;
Live 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          707 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          753 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 CAIGTIGICIGCAACACAIGACAGCCAIIGAAGCCIG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                818 C;
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fragments
                                                                                                                                                                                                                                                                                                                                                                                                                             637 A;
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22-OCT-1998.
16-APR-1998; U07694.
             WPI; 98-594562/
P-PSDB; W79260
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                                                                                     disorders
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DNA encoding coxackie virus and adenovirus receptor - useful for modulation of e.g. cardiac, pancreatic or gastrointestinal infection problem of e.g. cardiac, pancreatic or gastrointestinal infection Disclosure Fig 14. 10pp; English.

The present sequence encodes mouse coxsackievirus and adenovirus creceptor (CAR). The present invention also describes: (1) a method for receptor (CAR). The present invention also describes: (1) a method for modulates CAR protein activity or CAR nucleic acid expression, which modulates CAR protein activity of the cell in the absence of the agent; and (2) a sociated activity of the cell in the absence of the agent; and (2) a comprising contacting a biological sample with an agent capable of detecting CAR protein or mRNA such that the presence of CAR is detected.

Comprising contacting a biological sample with an agent capable of detecting CAR protein or mRNA such that the presence of CAR is detected.

Comprising contacting a biological sample with an agent capable of detecting CAR protein or mRNA such that the presence of CAR is detected.

Comprising contacting a biological sample with an agent capable of central nervous system, e.g. a non specific febrile illnection of the central nervous system, e.g. a non specific febrile illnection of the respiratory or gastrointestinal tract or childhood onset diabetes mellitus. Probes derived from CAR nucleic acids are useful for hybridisation assays, and antibodies raised against CAR include combining CAR protein and a candidate/test compound are useful in screening for drugs which interact with CAR protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               712 ACGATCGCGGGCGCGTCATAGGGACGCTGCTGGCCCTTGTGCTCATCGGGGCCATCCTC 771
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                                Locattor, 11. 1128

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/*trag= a
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/*trag= a stop codon, the sequence is shown as
continuing but gets unclear"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V62672 standard; CDNA; 4051 BP.
V62672;
15-FEB-1999 (first entry)
Tumour necrosis factor receptor related protein Tango-63d CDNA.
Tango-63d; tumour necrosis factor receptor related protein; human; apoptosis; cancer; autolmmune disease; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 1; Length 1128;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1998; U07694.
16-APR-1997; US-843652.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                   12.5EP-1997; U16189.
13.5EP-1996; US-026100.
(DAND) DANA FARBER CANCER INST INC.
BEF1961SON JM, Finberg RW, Hofowitz MS:
WPI; 98-207384/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
128. .1450
                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 TTCTGCTGICACAGGAAAGG 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.7%;
Local Similarity 62.5%;
hes 50; Conservative C
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diabetes mellitus; ss.
                                                                                                                                                                                                                            P-PSDB; W57213
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Best Local S
Matches 50,
               Mus sp.
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V62672
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PT disorders

Claim 5. Fig 1; 88pp; English.

This cDNA sequence includes a coding region for a new member of the This cDNA sequence includes a coding region for a member of the This cDNA sequence includes a coding region of Tango-634 i.e.

Tango-63d and Tango-63e (see V62673), were identified in a human prostate conNA library through EST sequencing and screening. The encoded polypeptides are identical with the exception of the encoded polypeptides are identical with the exception of the encoded polypeptides are identical with the exception of the markers WI-6088 and WI-653. A plasmid encoding Tango-63d send -36. Vectors containing these markers WI-6088 and WI-653. A plasmid encoding Tango-63d and -36. Vectors containing these morbiding Tango-63d and -36. Vectors containing these nucleic acid molecules, calls harboring recombined DNA encoding and/or -63e, fusion proteins that include Tando-63d and/or -63e, fusion proteins that include Tando-63d and/or -63e, methods are provided for the diagnosis and treatment of disorders associated with either an abnormally high or an canormally low rate of apoptotic cell death. Inhibitors can be conformally low rate of apoptotic cell death. Inhibitors can be conformally low rate of apoptotic cell death. Inhibitors can be conformed by a can be used for treating e.g. canocers, autoimmune disorders (e.g. systemic viral infections (e.g. herpesytiuses, poxituses, and adenoviruses).

C used for treating e.g. canocers, autoimmune disorders (e.g. systemic viral infections (e.g. herpesytiuses, poxituses, and adenoviruses).

C used for treating e.g. canocers, autoimmune disorders (e.g. systemic viral infections (e.g. herpesytiuses) poxituses, and adenoviruses of e.g. Alzhehmer's disease, parkinson's disease, amyotrophic lateral schemia or toxin-induced injury. In addition, T cell myculated diseases, including Albabatos septic shock, cerebral malaria, graft rejection, cytotoxicity, cachexia, and inflammation cerebral and screening assays.

C diagnosis and screening assays.

S equence 40
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resolute tumour. necrosis factor related proteins - used to develop products for the diagnosis and treatment of apoptosis-related disorders, e.g. cancers, autolmmune disorders or neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FBB-1999 (first entry)
Tumour necrosis factor receptor related protein Tango-63e cDNA,
Tango-632; tumour necrosis factor receptor related protein; human;
appoptosis; cancer; autoimmue disease; neurodegenerative disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%; Score 31; DB 1; Length 4051; 62.0%; Pred. No. 5.9; ative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Best Local Similarity 62.0%
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T02964/C
T02964 standard; CDNA; 580 BP.
AC T02064;
DT 01-MAR-1996 (first entry)
DF 01-MAR-1996 (first entry)
DF cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
KW Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
KW CR; gene therapy; transgenic animal; cancer; cell proliferation;
KW SS; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 GTCACCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTG 292
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                                                                                                                                                                                      Isolated tumour necrosis factor related proteins - used to develop products for the diagnosis and treatment of apoptosis-related disorders, e.g. cancers, autolmmune disorders or neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.5%; Score 31; DB 1; Length 3954; Best Local Similarity 62.0%; Pred. No. 5.8; Matches 49; Conservative 0; Mismatches 30; Indels
16-APR-1997; US-843652.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3744 TATAGTGTGTCACTCGTGG 3762
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                                                                              Holtzman D;
WPI; 98-594562/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9528483-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 GCAGTGGCCACTATGGGGTCTGGCCTGCTTGTCCTCCTTGACCCTCCTTGGCAGC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                        New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.

Claim 43; Pege B1-82; 109pp; English.

CDNA (702964) coding for the mouse cell-cycle regulatory (CCR) protein p15 (RB5118) was isolated from an embryonal carcinomal library using a probe based on a mouse CCR p13; 5 cDNA (702965).

The isolated cDNA can be used: to detect mutations in CCR genes that lead to cell proliferation; to breed transgenic animals to study cellular disorders involving CCR allele mutation, missypression; and to correct CCR-deficient cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V50430;
07-DEC-1998 (first entry)
Mouse coxsackievirus and Ad2 and Ad5 receptor (MCAR) cDNA.
MCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
Ad5 receptor; mouse; infection; vaccine; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.3%; Score 30.4; DB 1; Length 580; Best Local Similarity 57.3%; Pred, No. 4.1; Matches 55; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                               (COLD-) COLD SPRING HARBOR LAB.
Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
WPI; 95-373798/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 TCACATGGAACAGGGCCGGGTATGACTTTGCAACTG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 AGAAATGGTCCTTCGCCGGCCGTGAGATTGCTACAG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
157. .1215
/*tag= a
26-OCT 1995, U04636.
14-APR-1994; UG-227371.
25-MAY-1994; UG-227371.
14-SEP-1994; UG-3-06511.
29-MOY-1994; UG-3-16511.
(COLD-) COLD SPRING HARBOR LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V50430 standard; cDNA; 1301 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00-748-1998; 001724.
30-74N-1998; 001724.
30-7AN-1997; US-036986.
(UWRY ) UNIV NEW YORK STATE.
Philipson L. Tomko RP;
WPI; 98-437397/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (gene therapy).
Sequence 580 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 98-437397,
P-PSDB; W69698
                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; R85118
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V50430
         LOPERT PROPERTY OF THE PROPERT
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Claim 1: Page 1477; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp.
double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA ibraries prepared
from various human tissues; synthesis of cDNA was initiated from the-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 ACTITIGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 18; Page 17-20; 35pp; Japanese.

Rample 18: Page 17-20; 35pp; Japanese.

074052 is interleukin-1-beta cDNA and 074019-21 are primers used for the amplification of this cDNA. They are used specifically for the detection and isolation of this sequence. The primers have the advantage of high sensitivity and reliability and are useful in the pharmaceutical industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A primer for the detection and the determn. of a specific messenger RNA - can detect and determine specific mRNA(s) with high reliability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss. W09514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                      29-7AN-1996 (first entry)
Human interleukin-1-beta
Interleukin 1 beta; primer; mRNA; specificity; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 7.2%; Score 30; DB 1; Length 7824; Local Similarity 55.9%; Pred. No. 15; nes 57; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5899 CACTTATTCCCAGACAACCACCTTCTCCCCGCCCCCATCCCT 5940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 CIGGAATIGCTIGAAAAGCICTGCCTCCTCCTCCTCCCT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1905 C;
                                                                                                                                                                                                                                                                                                                                                            /*tag- a
/note- "N is undefined"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-1996 (first entry)
Human gene signature HUMGS05816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2099 A;
                                                                                                                                                                                                                                                                                                                                                                                                               J07123984-A.
16-MAY-1995.
05-NOY-1993; 275852.
05-NOY-1993; JP-275852.
(HTTB.) HITACHI CHEM CO LTD.
WPI; 95-211627/28.
                                                                                                   Q74052 standard; DNA; 7824
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11-NOV-1994.
12-NOV-1993. JP-355504.
(MATS.) MATSUBARA K.
(OKUBA.) OKUBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsubara K, Okubo K;
WPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                          misc_difference 1331
                                                                                                                                                                                                                                                                Homo sapiens.
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Matches
                                        RESULT
Q74052
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T23881/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRG: tumour necrosis factor related receptor; human; treatment; stroke; inflammation; arthritis; septicaemia; autoimmune disease; restenosis; transplant rejection; infection; ischemia; brain injury; bone disease; acute respiratory disease syndrome; acquired autoimmune disease syndrome; AIDS; cancer; atherosclerosis; Alzheimers disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding tumour necrosis factor receptor TR6 - and corresponding polypeptide, antibody, agonist, antagonist, etc claim 4: Page 25-27; 34pp: English.
This sequence encodes a novel human tumour necrosis factor related receptor, TR6. TR6 polypeptides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autorimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, infection, stroke, ischemmia, acute respiratory disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome) AlbS, bone diseases, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers disease. Sequence 3881 BP; 937 A; 922 C; 983 G; 1028 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 GICACCCICCACCAIGCAAGAICICAACACCAIGIIGICIGCAACACACAGCCAIIG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                              868 ACGATCGCGGCGCCGTCATAGGGACGCTGCTGGCCCTTGTGCTCATCGGGGCCATCCTC 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                    29 AGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCCTT 88
MCAR proteins or their fragments or variants are used to prevent or treat virus infections. Expressing the DNA in cells which lack these viral receptors renders the cells susceptible to transformation by adenoviral vectors carrying genes for gene
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Pred. No. 10;
0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                         Score 30.4; DB 1; Length 1301;
Pred. No. 5.7;
0; Mismatches 31; Indels 0
                                                                                                                                                                322 G;
                                                                                                                                                         327 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1997; 310562.
22-AUG-1997; US-916625.
14-WAR-1997; US-041230.
09-MAY-1997; US-85368.
(SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "TR6"
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                                                                                                                                                                355 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 GGCAGCTCACATGGAACAGG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         928 TICIGCIGICACAGGAACG 947
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59.58;
                                                                                                                                                                                                                                                            7.38;
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/*tag= 7
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25-JAN-1999 (first entry)
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.2'
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Conservative
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Best Local Similarity
Matches 47; Conserva
                                                                                                                                                                1301 BP;
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WPI; 98-523156/45.
P-PSDB; W76827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human TR6 cDNA.
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Gaps

2195 T;

1624 G;

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4283 CACTIATICCCAGACAACCACCTICICCCCGCCCCCAICCCT 4242
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P-PSDB; R94906.
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                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canaani D;
                                                                                                                                                                                                                                                                                                                                   misc_rna
                                                                         RESULT 13
T18696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IL-Ira BAC contiguous DNA sequence 96.
Tango-77; human; IL-Ira; cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-IR; regulation; sathma: rheumatoid arthritis; chronic myelogenous leukemains; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untrastated sequence is unique to a particular mRNA species, almost all the 3'-criented const hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 287 BP; 63 A; 55 C; 73 G; 81 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4343 ACTCTACAGCTGGAGGTAAGTGAATGCTATGGAATGAAGCCCTTCTCAGCCTCCTGCTAC 4284
                                                                                                                                                                                                                                                                                                                                               274 CAACACATGACAGCCATTGAAGCCTGTGTCCTTTGGCCCCGGGCTTTTGGGCCGGGGAT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 ACTITGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTC 178
                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  334 GCAGGAGGCAGGCCCCGACCCTGTCTTCAGCAGGCCCCCCACCCTCTGAGTGGCAAT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                       4327 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 14690; 20;
                                                                                                                                                                                                                                                                DB 1; Length 287;
                                                                                                                                                                                                                                                                                                       Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3299 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCT 220
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                                                                                                                                                                                                                                                                Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-1998; U16102.
02-UUL-1998; US-091650.
04-AUG-1997; US-054046.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
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a 14690 BP; 3810 A;
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X22303/c
ID X22303 standard; DNA; 14690 BP.
                                                                                                                                                                                                                                                           Query Match 7.2%;
Best Local Similarity 53.4%;
Matches 63; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 55.9 ies 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 99-153692/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-FEB-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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claim 2; Fig. 3; 29pp; English.

Claim 2; Fig. 3; 29pp; English.

A chord clone (7186795) codes for a novel radiation-protecting human checkpoint protein (894905), designated RAP-1, involved in requiration of cell cycle progression and/or apoptosis; It was captualtion of cell cycle progression and/or apoptosis; It was captualtion of cell cycle progression and/or apoptosis; It was captualtion of cell cycle progression and/or apoptosis; It was captualtion of cell cycle progression and immortalised in an immortalised captured progression and secret complemented UV sensitivity and was used to screen a captual progression or captured for early detection and prevention of tumour progression or can be used to design new drugs that enance radiotherapy or chemotherapy of diseases involving abnormal apoptosis.

Sequence 3510 BP; 974 A; 795 C; 848 G; 892 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1771 CACCGTCCCTCCATGGGAGAGCGAGAGAAAGATAACATCTCTATCCTCCTTCGA 1830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1831 TACCICCTIGGACTICICCCAAAGAAAACAAGAAAAAAGGAGAGATCTAGTIGGCAGCIT 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 CICCICITGACCCICCTIGGCAGCICACAIGGAACAGGGCCGGGIAIGACITIGCAACIG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New gene encoding a radiation protecting checkpoint protein - useful for diagnosis and treatment of cancer and other diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 CAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
V86356/c
1D V86365 standard; cDNA; 291 BP.
AC V86365;
DT 27-APR-1999 (first entry)
DE EST clone AR34.
KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "base n at position 3648 is not identified in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                             05-JUL-1996 (first entry)
RAP-1 radiation protecting checkpoint protein cDNA.
RAP-1; radiation protecting checkpoint protein; apoptosis:
cell death; cancer; diagnosis; therapy; radiotherapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHOS/) SHOSHAN H Z.
(UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.2%; Score 29.8; Best Local Similarity 51.9%; Pred. No. 13;
                                                                                                                                                                                                                                        Location/Qualiflers
       BP
                                                                                                                                                                                                                                                                                                      /*tag= a
31077. .3510
/*tag= b
/label= CDNA3
T18696 standard; cDNA; 3510
T18696;
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11-0CT-1994; IL-111238.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding human secreted proteins - derived from
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
provary, pituitary, retina and colon cDNA libraries
claim 1: page 210: 633pp; Engilah.

This sequence represents an expressed sequence tag (EST), and is a
rise contect of the invention. The polynucleotides of the invention are
colonical expressed sequences isolated from a variety of human tissue
sources. The EST sequences isolated from a variety of human tissue
cources. The EST sequences and proteins encoded by them are preditted to
treating, preventing or ameliorating medical conditions in humans and
animals, although no supporting data is given. Suggested activities
conditional activity, immune stimulating or suppressing activity,
cactivin/inhibin activity, chemotactic/chemokinetic activity,
activin/inhibin activity, receptor/ligand activity, anti-inflammatory
cactivity, cadherin/tumour invasion suppressor activity, tumour invasion suppressor activity, tumour invasion suppressor activity, tumour inhibition
activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemotaxis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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Werster ....
Werster ....
Werster ....
Werster ....
Wer isolated Treponema pallidum nucleic acids - used to develop
New isolated Treponema pallidum nucleic scharacterisation, prevention
and therapy of T. pallidum infections, particularly syphilis
Claim 1; Page 661-672; 1150pp; English.
X50500-21243 represent polynucleotides sequences from the genome of
Treponema pallidum. The sequences can be used for detection,
diagnosis, characterisation, prevention and therapy for T. pallidum
infections, particularly syphilis. They can also be used for detecting
diseases related to Borrelia infections in animals, and for the
production of blosynchetic products such as enzymes.
Sequence 20757 BP; 4912 A; 6068 C; 5301 G; 4457 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 29.8; DB 1; Length 291; 70.2%; Pred. No. 4.7; tive 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                10-APR-1998; U06954.
10-APR-1997; US-835913.
(GEXT) GENETICS INST INC.
AGOSTINO MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
Racie Lia, Spaulding V, Treacy M;
WPI: 99-070076/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X20599 standard; DNA; 20757 BP
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24-JUN-1997; US-050667.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 A;
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Best Local Similarity 70.2'
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 BP;
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X20599/
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                                                                                         NAMES OF STREET OF STREET
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7.28;

Query Match Best Local Similarity

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                                                                                288 CATIGAAGCCIGIGICCTICITGGCCCGGGCTTTTGGGCCGGGGAIGCAGGAGGCAGGCC 347
                   228 CCAGCGTCACCCTCCACCATGCAAGATCTCAACACCCATGTTGTCTGCAACACATGACAGC 287
 Gaps
 ö
  Indels
                                                                                                                            348 CCGACCCTGTCTTCAGCAGGCCCCCCACCCTCCTGAGTGGC 388
  82;
 Mismatches
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0
    Conservative
    79;
    Matches
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search completed: March 20, 2000, 09:32:31 Job time: 1114 sec

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Sequence 1, 1 Sequence 1, 1 Sequence 1, 1 Sequence 3, 1 Sequence 3, 2 Sequence 3, 2 Sequence 1, 2 Sequence 1, 2 Sequence 1, 2 Sequence 1, 3 Sequence 1, 5 Sequence 2, 5 Sequence 3, 5 Se

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4 GGGACTICAGIGICICCICCATCCCAGGAGCGCAGIGGCCACIAIGGGGICIGGGCIGCC 63
PCT-US93-06251-65
US-07-914-281-1
US-08-393-246-1
US-08-373-411-4
US-08-273-411-4
US-08-250-858-3
US-08-250-858-1
US-08-446-915-3
US-08-744-11
US-08-744-11
US-08-744-11
PCT-US91-00699-1
PCT-US95-06639-3
                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: V.T.Y.
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEDUTION FOR SEQ ID NO: 14:
SEDUTION FOR SEQ ID NO: 14:
SEROIT 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Innear
     ; CLONE: PTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: VA
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US-08-232-463-14
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Sequence 7, Appl
Sequence 1, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 2, Appl
                                                                                           March 18, 2000, 16:07:56; Search time 61.26 Seconds (without alignments) 811.048 Million cell updates/sec
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                                                                                                                                                                           1 ACCGGGACTTCAGTGTCTCC......AAAATTCGGTATGCTGAATT 415
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                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
/cgn2_6/ptodata/2/lna/5B_COMB.seq:*
/cgn2_6/ptodata/2/lna/5C_COMB.seq:*
/cgn2_6/ptodata/2/lna/5C_COMB.seq:*
/cgn2_6/ptodata/2/lna/5C_COMB.seq:*
/cgn2_6/ptodata/2/lna/5C_COMB.seq:*
/cgn2_6/ptodata/2/lna/PcCTUS9_COMB.seq:*
/cgn2_6/ptodata/2/lna/PcTUS9_COMB.seq:*
                   GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-1467-781-3
US-08-125-487-3
US-08-674-887A-5
US-08-674-887A-5
US-08-312-766A-31
US-08-937-466-1
US-08-937-466-1
US-08-937-466-1
US-08-937-46-1
US-08-93-110-2
US-08-93-110-2
US-08-93-110-2
US-08-94-168-1
US-08-68-33-110-2
US-08-749-168-1
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US-08-466-390-3
US-08-470-950-3
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US-08-938-365-1
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US-08-646-715-10
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US-07-669-171-1
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US-07-709-949-1
                                                                                                                                                                                                                               214294 seqs, 59861208 residues
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                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                          US-09-092-296-7_COPY_5_419
415
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                           COMPUTE: USA
ZIF: 22313-0293
ZIF: 22313-0293
ZIP: 22313-029
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: BR C COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NATE:
CLASSIPICATION: 435
PRIOM APPLICATION NATE:
APPLICATION NUMBER: US/07/935,313
Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: RALEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPAN: (703)836-9300
TELEPAN: (703)836-9300
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; NAME/KEY;
; LOCATION:
PCT-US95-04636-7
                                           Query Match
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124 GCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTTCCTGGA 183
                                                                                                                                                                                              184 ATTGCTTGAAAAGCTCTGCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCA 243
                                                                                                                                                                                                                                                                     244 CCAIGCAAGAICTCAACACCAIGTIGICIGCAACACAIGAGCCAIIGAAGCCIGIGIC 303
                                                                                                                                                                                                                                                                                                                                            304 CITCTIGGCCCGGGCTITIGGGCCGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTCA 363
                                                   64 CCTIGICCICCICTIGACCCICCTIGGCAGCICACAIGGAACAGGGCCGGGIAIGACTIT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08627610
Partent No. 5919997
Partent No. 5919997
Partent No. 5919997
Partent Description
PapelloANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Definho, Ronald A.
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Regulation
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USER
ZIP: D2109
ZIP: D2109
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: ASCII(text)
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: 04-APR-196
CLASSIETCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, NEVERMATION:
TELEPHONE: (617) 227-74
INFORMATION FOR EQUID IN:
TELEPHONE: (617) 227-74
INFORMATION FOR EQUID IN:
TELEPHONE: (617) 227-5941
INFORMATION FOR EQUID IN:
TELEPHONE: (617) 227-74
SEQUENCE CHARACTERISICS:
LENGTH: 580 base pairs
TYPE: ULGARACTERISICS:
LENGTH: 580 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                          1415 YYYYYYYYYYYYYYYYGTACCAA 1441
                                                                                                                                                                                                                                                                                                                                                                                                                     364 GCAGGCCCCCACCTCCTGAGTGGCAA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 60 State Street
CITY: Boston
STRIE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
: LOCATION: 91..480
US-08-627-610-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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US-08-627-610-7/c
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                                                  Gaps
                                                                                                                                            128 GCGGTGGCCAGGCCCGCGTCACTGCTGCCCCCAACATGCCCTTGTCCCCGGTCTGTGGC 69
                                                                                         35 GCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCTTGACCCTCCTTGGCAGC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US95/04636
FILING DATE:
7.3%; Score 30.4; DB 4; Length 580; 57.3%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.3%; Score 30.4; DB 6; Length 580;
Best Local Similarity 57.3%; Pred. No. 1.4;
Matches 55; Conservative 0; Mismatches 41; Indels
                                               0; Mismatches 41; Indels
                                                                                                                                                                                         95 TCACATGGAACAGGGCCGGGTATGACTTTGCAACIG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 TCACATGGAACAGGCCGGGTATGACTTTGCAACTG 130
                                                                                                                                                                                                                        68 AGAAATGGTCCTTCGCCGGCCGTGAGATTGCTACAG 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFCATION:
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DAIE: 25-MAY-1994
RIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 7:
ENGURACION NOW. 7:
LENGTH: 580 base pairs
                                                                                                                                                                                                                                                                                                                                     PCT-US95-04636-7/c; Sequence 7, Application PC/TUS9504636; Settlement Internation; APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-08-817-436A-1
; Sequence 1, Application US/08817436A
             Best Local Similarity 57.38
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
91..480
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APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Comai, Lucio
APPLICANT: Boy, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Nack
APPLICANT: Wang, Edith
APPLICANT: Weinstein, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NGEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SOUTHERS: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLERK, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 ICCTGGAATIGCTIGAAAAGCTCTGCCTCCTCCATCTCCCTTCAGGGACCAGCGTCA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 CCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCAT 290
APPLICANT: MERMIN, JUNE RAE
TITLE OF INVENTION: TGP-bJ/b2: A NOVEL CHIMERIC TRANSFORMING
TITLE OF INVENTION: GROWTH FACTOR-BETA
NUMBER OF SEQUENCES: 3
ADDRESSEE: ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.0%; Score 29.2; DB 1; Length 1560; Best Local Similarity 53.5%; Pred. No. 5; Matches 61; Conservative 0; Mismatches 53; Indels 0
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/O7/669,171
FILING DATE: 19910314
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 564-159-999
TELEPOMMUTCATION INFORMATION:
TELEPRAX: 212-790-909
TELEPRAX: 212-786-9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TELENT: MATERIALISS:
TELENT: 1560 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08188582
Patent No. 5534410
GENERAL INFORMATION:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: 261..1430
US-07-669-171-1
                                                                                                                                                                             E: N.Y.
TRY: U.S.A.
10036
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                                                                                                                                                       CITY: NE
STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 CAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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            TITLE OF INVENTION:

APPLICANT: Canamani, Dan
TITLE OF INVENTION: Human Checkpoint Gene and Gene for
TITLE OF INVENTION: Antisense RNA thereof
TITLE OF INVENTION: Antisense RNA thereof
ORRESPONDENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wigman, Cohen, Leitner & Myers
STREET: 900 17th Street, N.W., Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch, 1.44Mb storage
COMPUTER: IBM compatible
ORPERATING SESTEM: DOS
SOUTHWARE: ASSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Home sapiens CELL LINE: ESTABLISHED XERODERMA PIGMENTOSUM GM2096-SV3 IMMEDIATE SOURCE: CLONE: RAP-1 CDNA
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCLI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,436A
FILING DATE: 11-UNN-1997
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12445
FILING DATE: 11-OCT-1995
ATTORNEY/AGENT INFORMATION:
FILING DATE: 11-OCT-1995
ATTORNEY/AGENT INFORMATION:
REGISTATION NUMBER: 25,109
REFERENCE/DOCKET NUMBER: 0744.066
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-463-7700
TELEPHONE: 202-463-7700
TELEPHONE: 202-463-750
TELEPHONE: 202-463-750
TELERAN: 202-463-770
TELERAN: 3099 base pairs
TYPE: NUCLEIC acid
TYPE: NUCLEIC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/07669171
Patent No. 5304541
GENERAL INFORMATION:
APPLICANT: PURCHIC, ANTHONY F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11near MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.2 Best Local Similarity 51.9 Matches 67; Conservative
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1891 AAACGGAGG 1899
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US-08-098-141-1
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sequence 10, Application Us/08646715

Patent No. 5637666

SEMERAL INFORMATION:

APPLICANT: Tilan, Robert

APPLICANT: Comal, Lucio

APPLICANT: Dilact, Brian D.

APPLICANT: Hoey, Timothy

APPLICANT: Ruppert, Siegfried

APPLICANT: Wang, Edith

APPLICANT: Weinzierl, Robert O.J.

TILE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,

TILLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,

TILLE OF INVENTION: NUCLEIC ALIBER OF SERVINGENCE ADDRESSE: SEERR, HOHBACH, TEST, ALBRITTON & HERBERI

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3947 TGGAAGGTGGCGCATTTGTTTGATAAAAGAGGGGCAGAATTTGTTAGTCGTCTCATGTGTC 3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4007 CATTATGAATGACTGTCTTTTCCAACTCCTCCTGTTCTTCTGTCATGGCAACAGGT 3948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 AACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 CACTATGGGGTCTGGGCTGCCCTTGTCCTCTTGACCCTCCTTGGCAGCTCACATGG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 CTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.0%; Score 29.2; DB 1; Length 5962;
47.8%; Pred. No. 8.9;
tive 0; Mismatches 93; Indels 0
                                                                                                                                                                           CURRENT SYSTEM: NC-LOS/RS-LOS
SOFTHARE: PREEDIN RC-LOS/RS-LOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Osman, Richard A REGISTRATION NUMBER: 36.627
REFERENCE/DOCKET NUMBER: 36.627
REFERENCE/COCKET NUMBER: 36.627
REFERENCE (14.55) 398-3249
TELEX: 910.277299
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 5962 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Innear
                                       COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.8
Matches 85; Conservative
San Franciaco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: CDS
; LOCATION: 14.5692
US-08-188-582-10
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12D: 9111-412

COMPUTER READMLE FORM:

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WEDUTUR FREADMLE FORM:

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1120 cgcctcaccgccggcctcatcgtcgtcgtggtggtcgtggtggcctcgtcgtcggc 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
5185254-3
; PATCHIN . 5185254
; APPLICANT: LINNERBACH, ALBAN
; TITLE OF INVENTION: GENE FAMILY OF TUMOR-ASSOCIATED ANTIGENS
; NUMBER OS SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/291,583
FILING DATE: 29-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.0%; Score 29; DB 1; Length 1157;
54.1%; Pred. No. 5;
Ive 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 7.0%; Score 29; DB 7; Length 2259; Best Local Similarity 52.0%; Pred. No. 6.8; Matches 65; Conservative 0; Mismatches 60; Indels
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                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_signal
LOCATION: 62.119
LOCATION: NAME/KEYIN: PUBLICATION: NATHORMATION: AUTHORS: McLean, J W JOURNAL: Journal of Biological Chemistry
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1157 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: double TYPE: TYPE: ACID STRANDEDNESS: double TYPOLGUE TYPE: CDN to MANA HYPOTHETICAL: NO ANTI-SENSE: NO FRAGENT TYPE: N-terminal ORIGINAL SOURCE: ORIGINAL SOURCE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.0%;
Best Local Similarity 54.1%;
Matches 59; Conservative '
                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 62.1015
FEATURE:
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1984
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Pattent No. 5472858
GENERAL INFORMATION:
APPLICANT: Attle, Alan D
APPLICANT: Gretch, Daniel G
APPLICANT: Stephen L
TILE OF INVENTION: Production of Recombinant Proteins in TILLE OF INVENTION: Production of TILLE OF INVENTION: Insect Larvae
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles 6 Brady
STREET: P.O. Box 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 7.0%; Score 29; DB 1; Length 3060; Best Local Similarity 50.4%; Pred. No. 7.7; Matches 71; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70; Indels
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APPLICATION NUMBER: US/07/709,949
FILING DATE: 19910604
        TLLING DALE:

CLASSIFICATION: 435

ATORNEY/AGENT INFORMATION:
NAME: KAPLAN BSQ., Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: 092662-001
TELEPHONE: 617:27-5020
TELEPHONE: 617:27-566
INFORMATION FOR SED ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 3060 base pairs
TYRE: nucleic acid
STRANDENESS: single
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ATORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9629691801
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION: (608) 251-5000
TELEPROMICE: (608) 251-5000
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ZIP: 53701-2113
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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  FILING DATE: 19930723
                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-098-141-1
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US-07-709-949-1
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COMPUTER READABLE FORM:
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Patent No. 5686562
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
MODRESSE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
US-08-750-357-8/c

| Sequence 8, Application US/08750357
| Patent No. 6006437
| Patent No. 6006437
| GENERAL INFORMATION:
| APPLICANT: WILLIAMS, Mark
| APPLICANT: WILLIAMS, Mark
| APPLICANT: WILLIAMS, MARK
| TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
| TITLE OF INVENTION: MALE STERILE PLANTS
| WUMBER OF SEQUENCES:
| CORRESPONDENCES:
| ADDRESSEE: BURNS DOANE, SWECKER & MATHIS, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.9%; Score 28.6; DB 5; Length 2662; Best Local Similarity 61.3%; Pred. No. 9.7; Matches 46; Conservative 0; Mismatches 29; Indels 0
                                                                                                                                                                                                                       CORRESOURNE ALEACTOR.

ADDRESSE: ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREE: P.O. Box 1404
CITY: Alexandria
COUNTRY: United States
2 IP - 23313-1404
COMPUTER: EADABLE FOR STEME: PC-DOS/MS-DOS
OCHWATER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,357
FILING DATE: 21-MAR-1997
CLASSIFICATION NUMBER: US/08/750,357
FILING DATE: 12-MAR-1997
CLASSIFICATION NUMBER: 01907
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-620
TELEPHONE: ASC ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGHATION FOR SEC ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGHATION FOR SEC ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 02110
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US-08-466-390-3/c
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4668 CIGCIGCIGCACCTIGCIGGCTIGGICAGAGICAGCCAGITICIIACICAGITCTICCAG
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APPLICANT: INCORMITON:
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBERULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 6306;
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Best Local Similarity 46.1%; Pred. No. 16;
Matches 95; Conservative 0; Mismatches 111; Indels
COMPUTER: IBW PC compatible
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/466,390
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
FILING DATE: NOWER: A75
ATTONNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: AP-013
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS: CLEVELAND, DON W
TITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
TITLE: PROPERIN THAT DEFINES A NOVEL PATHWAY FOR
JULIE: SEGREGATION OF PROFEINS AT MITOSIS
JOURNAL: J. Cell Biol.
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Sequence 3, Application US/08470950
Patent No. 5698439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..6306
PUBLICATION INFORMATION: A
AUTHORS: COMPTON, DUNNE A
AUTHORS: SZILAK, ILYA
AUTHORS: CLEVELAND, DON W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VOLUME: 116
PAGES: 1395-1408
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US-08-466-390-3
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4608 creescaercaerricrecererrecressaaccerecerecerecaesacerres 4549
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46.1%; Pred. No. 16;
Live 0; Mismatches 111; Indels 0;
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUTHORS: CLEVELAND, DON W
TITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
TITLE: PROPEIN THAT DEFINES A NOVEL PATHWAY FOR
JUTILE: SEGREGATION OF PROTEINS AT MITOSIS
JOURNAL: J. Cell Blol.
                                                                                                                                                                                                                                                                                                              CORPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IRM PC Compatible
COMPUTER: IRM PC Compatible
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,781
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
RECISTRATION NUMBER: 27,829
TELEPHONE: (617) 248-700
TELEPHONE: (617) 248-700
TELEPHONE: (617) 248-7100
INFORMATION FOR ESO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                        ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 125 HIGH STREET
CIITY: BOSTON
COUNTRY: WAA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4548 CTTGGCACCCTCATACTTGGCAGTCA 4523
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LOCATION: 1..6306
PUBLICATION INFORMATION:
AUTHORS: COMPTON, DUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 95; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
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; DATE: 1992
US-08-467-781-3
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US-08-195-487-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LUCATION: 1..6306
PUBLICATION INFORMATION:
AUTHORS: COMPTON, DUNNE A
AUTHORS: SILAK, ILYA
AUTHORS: CLEVELAND, DON W
TITLE: PRIMARY STRUCTURE OF NUMA, AN INTRANUCLEAR
TITLE: PROPERIY THAT DEFINES A NOVEL PATHWAY FOR
JOURNAL: J. Cell Biol.
VOLUME: 116
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMM PC compatible
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/08/470,950
FILNS DATE: 06-JUN-1995
CLASSIFICATION: 36
ATTORNEY/AGENT INFORMATION:
NAME: PTTCHER ESQ. EDMUND R
REGISTRATION NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: (617) 248-7100
TELEFAK: (610) 24
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US-08-467-781-3/C
15-64467-781-3/C
5-94467-781-3/C
5-94467-781-3/C
6EMERAL INFORMATION:
7 APPLICANT: TOURATLY, GARY
7 APPLICANT: LIDGARD, GRAHAM P
       : 125 HIGH STREET
BOSTON
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PAGES: 1395-1408
NATE: 1992
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                                                                                                                            USA
                                                                                                                            COUNTRY: US
ZIP: 02110
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Sequence 3, Application US/08195487

Patent No. 5783403

GENERAL INFORMATION:
APPLICANT: TOKENTY, GARY
ITILE OF INVENTION:
ITILE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA HURWITZ & THIBEAULT
STREET: 53 STATE STREET
COTTY: BOSTON
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LOCATION: 1..6306
LUCCATION: 1..6306
PUBLICATION INFORMATION:
AUTHORS: COMPTON, DONNE A
AUTHORS: SILLAK, ILLYA
AUTHORS: CLEVELAND, DON W
TITLE: PROFEIN THAT DEFINES A NOVEL PATHWAY FOR
TITLE: PROFEIN THAT DEFINES A NOVEL PATHWAY FOR
TITLE: SEGRECATION OF PROTEINS AT MITOSIS
JOURNAL: JOURNAL OF CELL BIOLOGY
VOLUME: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,487
FILING DATE:
CLASSIFICATION NUMBER: US/07/901,701
FILING DATE:
APPLICATION NUMBER: 27,829
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 27,829
FILING DATE:
TELEFANTION NUMBER: 27,829
FILING DATE:
TELEFANTION NUMBER: ATP-013
TELEFANTION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6306 base pairs
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STRANDENESS: AINGLE
TYPE: NOTICE CHARACTERISTICS:
LENGTH: 6306 base pairs
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FRGES: 1195-1408
; DATE: MAR-1992
US-08-195-487-3
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                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: BOSTO
STATE: MA
COUNTRY: US
ZIP: 02109
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Oy 368 GCCCCACCCCGAGGGGCAATAA 393
Db 4548 CTTGGCACCCCATACTTGGCAGTCA 4523
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Search completed: March 18, 2000, 16:08:09 Job time: 693 sec 90-est31:*
90-est32:*
90-est32:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                      March 19, 2000, 08:56:37; Search time 538.4 Seconds (without alignments) 2910.291 Million cell updates/sec
                                                                                                                                             US-09-092-296-7_COPY_5_419
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1 ACCGGACTICAGIGICICC......AAAAIICGGIAIGCIGAAIT 415
          GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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                                                            OM nucleic - nucleic search, using sw model
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Perfect score:
Sequence:
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em_gss2:* em_gss3:*

A1857998 wj69b01.x A0718761 Hg_5511_B T94049 ye33£07.x1 A1136523 UI-R-C2P-A1010074 ESP204625 A1535315 UI-R-C3-S AL076960 Drosophil

A1857998 AQ718761 T94049 A1136523 A1010074 A1535335 CNSO0K09

61 44 73 74 74 74 74

404 552 176 328 190 201

Description

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Length

SUMMARIES

em_gss9:* em_gss10:* gb_gss10:* gb_gss10:* gb_gss12:* gb_gss12:* gb_gss12:* gb_gss13:* gb_gss14:*

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Entranged Metazoa: Chordata; Craniata; Vertebrata; Mammalla; Entraria: Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 4040, 1040, 1040, 1040, 1040).

E 1 (bases 1 to 4040, 1040, 1040, 1040).

S NCI-CGAP http://www.ncbl.nlm.nlh.gov/ncicgap.

NoticGAP http://www.ncbl.nlm.nlh.gov/ncicgap.

Tumor Gene Index

U Upublished (1997)

Tumor Gene Index

U On Jun 5, 1988 this sequence version replaced gi:3189004.

Contact: Robert Strausberg h.b.D.

Tel: (301) 496-1550

Emmil: Robert Strausbergenih.gov

Tasue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lini.gov/bbrp/image/image/image.html
AA282040 Z889a03.8

AA534569 INT7C11.8

AA741185 DA3002.5

AA936790 OA89a02.8

AA936750 OA89a02.8

AA417974 Z297C08.8

AA417974 Z297C08.9

AA417974 Z297C08.9

AA509652 HSCIQCIOI OCOSOPII

AA243870 ZC65404.8

AA765420 WX76C1.X

AA766413 DZ586915

AA766439 DZ76C04.8

AA766413 DZ76C04.8

AA766413 DZ76C04.8

AA766413 DZ76C04.8

AA766413 DZ76C07.8

AA86267.2

AA8627.2

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Information can be
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sapiens cDNA Clone IMAGE:2408041 3',
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A1829206
AA243870
AA376266
AA76639
AA76643
AA76578
AA1632159
AA163524
AA163524
AA162544
AA16254
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AW013553
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AA830716
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AI926123
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wj69b01.x1 NCI_CGAP_Lu19 HOMO
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   mRNA sequence.
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 ACCESSION
VERSION
KEYWORDS
SOURCE
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LOCUS
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AUTHORS
TITLE
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;
Eutherla; Frinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 552)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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HS_5511_B2_F09_77A RPCI-11 Human Male BAC Library Homo saplens
aponduc clone Plate=1087 Col=18 Row=L, genomic survey sequence.
AQ718761
AQ718761.1 GI:5468077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 ATGAGTCCAGCTTCCIGGAATTGCTTGAAAGCTNTGCCTCCTCCTCCTCCATCTCCTCAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          105 CAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 ATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 GGACCAGCGTCACCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGAC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 AGCCATTGAAGCCTGTGTCCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAG 344
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                                                                                                                                                                                                                                                                                                                                                      61; Length 404;
                                                                                                                                                                                                                                                                                                                                                     74.3%; Score 308.4; DB 61; Length 99.4%; Pred. No. 7.2e-79; 1ve 0; Mismatches 2; Indels
Seq primer: -40UP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 196
High quality sequence stops: 155 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoëimaqe.llni.gov) for further information.
Insert Length: 196 Std Error: 0.00
Seq primer: Mi3RPl
High quality sequence stop: 155.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Pred. No. 4.5e-34;
0; Mismatches 6;
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Best Local Similarity 96.2%;
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Rattus norv
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                                 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu, Clones may be purchased from
BACPAC Resources (http://pacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1087
Seg primer: 77
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m c} 124 g 117~{
m t} 17 others
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ye33f07.rl Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:119557 5', mRNA sequence.
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Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176)
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="Plate=1087 Col=18 Row=L"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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/db_xref="taxon:9606"
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T94049.1 GI:727537
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Best Local Similarity 89.29
Matches 165; Conservative
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human.
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AI535335
AI535335.1 GI:4449470
       AI010074.1 GI:3223906
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Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
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//dab_nost="DB108 (Life Technologies)
//dab_nost="DB108 (Life 
451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 315 8250 8250 Fax: 319 315 956 8250 Exail: 319 315 9565 Email: msoares@biue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Lung library. CDNA Library Preparation: M. Fatima Bonaldo, Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used as a driver in a hybridization with the UT-R-CI
library in the form of single-granded circles. The
remaining slingle-stranded circles (subtracted library) was
purified by hydroxyapatte column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-C2p library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
77c 98 g 91 t
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EST704525 Normalized rat lung, Bento Soares Rattus sp. cDNA clone
RLUBT38 3' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="UI-R-C2p-nq-e-02-0-UI"
/clone_lib="UI-R-C2p"
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                   Seq primer: M13 Forward.
Location/Qualifiers
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Norway rat.
Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 201)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
Rattus sp.
Rattus sp.
Rattus sp.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 190)
Lee, M.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Rerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Fax: 319 335 9565 Email: msoarces@blue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 TCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGCAAGATCTCAACACCATGTTG 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..190
/organism="Rattus sp."
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/clone_Ilb="Normalized rat lung, Bento Soares"
/note="Organ: lung; Vector: pT/T3Pac; Site_1: EcoRI;
Site_2: Not!"
51 c 59 g 41 t
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                                                                                                                                                                                                                                                               Gene Index
Unpublished (1998)
On Jan 19, 1998 this sequence version replaced g1:2150555.
Contact: Lee, NH
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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65.1%; Pred. No. 0.0019;
tive 0; Mismatches 37; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
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97044477
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AAZ82040 331 bp mRNA EST 14-AUG-1997 z889a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704620 3',
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NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 CCCCTTGTCCTCCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TIGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                862 VKISYVCIBICVMTMCWTVMHTAAADACMAMMMANASACAVYVMTTTIGSSSCGCGVGTK 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 GAATTGCTTGAAAAGCTCTGCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCTC 241
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                                                                                                                                                                                                                                                                                                                                                                                                      9.0%; Score 37.4; DB 79; Length 1101; 19.6%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                  489 others
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                                                                                                                                                                                                                                                                              /organism="brosophila melanogaster"
/db.xref="taxon:722"
/clone_llb="RCI-98"
/clone="BACR39004"
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AA282040
AA282040.1 GI:1924872
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                                                                                                                               oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Seq primer: Mi3 Porward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 TCCCTTCAGGGACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCA 275
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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53.0%; Pred. No. 0.1;
Ive 0; Mismatches 37; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 GAGCCTGAGAGCAGCTGGGCTGGGCCTGGAGCG 102
                                                                                             /organism-"Rattus norvegicus"/strain-"Sprague-Dawley"/db_xref-"taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.8%;
Best Local Similarity 63.0%;
Matches 63; Conservative
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/Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="lwAGE:92540"
/clone="lwBoled"
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/
   cDNA Library Preparation: N. Bento Scares, Ph.D. cDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consorthum/LLNL at:
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 GCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 424)
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Unknown library type
Insert Length: 742 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 387.
Location/Qualifiers
1. 424
/organis="Homo sapiens"
/db.xref="taxon:9606"
/db.xref="taxon:9606"
/db.xref="taxon:9606"
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                                                                                                                                                                                                                                  Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 370.
Iocation/Qualifiers
                                                                                                                                                                        www-bio.llni.gov/bbrp/image/image.html
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                                                                                                                                                         Email: Nobert_Sruubberg@nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
IMBGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m3 fwd. Er from Amersham
High quality sequence stop: 242.
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I (bases 1 to 494)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Talin: Robert Strausbergenih.gov

Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1402231.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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/organism='Homo sapiens'
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/tissue_Iype='germinal center B cell'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36.4; DB 31;
Pred. No. 2.3;
0; Mismatches 51;
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AA534569
AA534569.1 GI:2278822
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Best Local Similarity 56.8%;
Matches 67; Conservative
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A1018775/c
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Eutherla: Primates; Catarrhini; Hominidae; Homo.

I (Basea I to 402)

NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tunor Gene Index

In Unpublished (1997)

On Jan 17, 1998 this sequence version replaced gi:2045507.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: N. Bento Soares, Consciting Center

Clome distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNI at:

www-bio.llnl.gov/bbrp/image.html
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oh89a02.s1 NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1474154 3',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Kid5"
/tissuc_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                 Query Match
8.8%; Score 36.4; DB 38; Length 424;
Best Local Similarity 56.8%; Pred. No. 2.5;
Matches 67; Conservative 0; Mismatches 51; Indels 0;
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 386.
Location/Qualifiers
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/clone="IwAGE:1474154"
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cDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-CGAP clone distribution information can be
found through the 1.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/lmage/lmage.html
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A1018775 A1018775.1 G1:3232573
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1 (bases 1 to 529)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

Unpublished (1997)

On Jan 14, 1998 this sequence version replaced gi:1797652.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 466-1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
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                                                                                                                                                                                                                                                    ch 8.8%; Score 36.4; DB 40; Length 402; 1 Similarity 56.8%; Pred. No. 2.5; 67; Conservative 0; Mismatches 51; Indels 0.
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/clone=Lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH108"
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Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence Stop: 451.
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EST2293941 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
RGIBSZ27 5' end, mRNA sequence.
AW143645 GI: GI:6163544
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1. (bases 1 to 354, 1 to 364, 1 t
                                                                                                                                                                                                                                133 GCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGA 192
                                                                                                                                                                                                                                                                The Institute for Genomic Research 7972, Medical Center Drive, Rockville, MD 20850, USA 7972, Medical Center Drive, Rockville, MD 20850, USA 7972, Medical Center Drive, Rockville, MD 20850, USA Eax: (301)-838-0208
Fax: (301)-838-0208
For inne availability, additional sequence and expression Information related to this EST please check the TIGR Rat Gene Contact the ATCC (http://www.atcc.org/atcc.html). To order a clone Seq primer: MI3 Reverse.
                                                                                                                                                                                                Gaps
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/note="Vector: pT/T3Pac; Site_1: EcoRI; Site_2: NotI"
76 c 82 g 90 t
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                                                                                                                                                                                                                                                                                                                                                                                       239 AACTGTGGCCATGCATTTTTTTTTTTTTTAAGACCAGTGTGATAGTAGTAGCCATGCA 182
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                                                                                                                                   Length 529;
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8.6%; Score 35.6; DB 70; Length 354;
Best Local Similarity 45.9%; Pred. No. 4;
Matches 122; Conservative 0; Mismatches 144; Indels 0;
                                                                                                                                                                                      51; Indels
                                                                                                                      Score 36.4; DB 41;
Pred. No. 2.7;
0; Miamatches 51;
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            165
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/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGIBX27"
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            104
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8.8%;
Best Local Similarity 56.8%;
Matches 67; Conservative
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Rattus sp.
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/note="Organ: mixed (see below); Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHw, pregnant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDKaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutherist, Frimates; Catarrhini; Hominidae; Homo.

Eutherist; Frimates; Catarrhini; Hominidae; Homo.

I (bases 1 to 537)

RS Hiller,L., Allen,M., Bowles,L., Dubuque,T., Gelsel,G., Jost,S., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marria,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Wihite,Y., Walle,T., Waterston,R. and Wilson,R. Tan,F., Theising,B., WashU-Merck EST project 1997

AL Ompublished (1997)

On Sep 12. 1996 this sequence version replaced gi:1393089.

Ashington University School of Medicine

Washington University School of Medicine

Tal: 314 286 1800

Email: est'ewatson wustl.edu

This clone is available royalty-free through Link; contact the INAGE Consortium (infedimage.linl.gov) for further information. Possible reversed clone: similarity on wrong strand seq primer: -41mi3 fwd. ET from Amersham

High quality sequence stop: 502.

urce

L. 337
                                                                                                                                                                                                                                                                                                                                                                                                                                       AA417974 537 bp mRNA EST 16-OCT-1997
zv97c08.s1 Soarse_NhHWL_S1 HOmo sapiens cDNA clone IMAGE:767726 3'
sinilar to WP:FS9B2.3 CE00231 N-ACETYL-GLUCOSAMINE-6-PHOSPHATE
DEACCETYLASE; ', mRNA sequence.
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/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                    8 TCTTTAATGAATGGTCTTGCGTTTGAGGCGCCGGGAAAAGGCGGGATAGGTAGAACGCCT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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/db_xref="taxon:9606"
/clone="IMAGE:767726"
                                                                                                                                                                                                              358 CTTTCAGCAGGCCCCCACCCTCCTGA 383
                                                                                                                                                                                                                                                   /lab_host-"DH10B"
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//Lab_nogt="Dist_Sozes_NFL_TGBC_SI"
//Lab_nogt="Dist_Sozes_NFL_TGBC_SI"
//Lab_nogt="Dist_Side_I") Not I; Site_I: Eco RI;
a modified polylanker; Site_I: Not I; Site_I: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.G.E. clones 297480-302087, 692632-687239,
726408-72871, and 729086-731399, Subtraction by Bento
Soares and M. Fatima Bonaldo.
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Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2150675.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1150

Email: Robert_Strausberg enih.gov
This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@thingor.inin.gov) for further information. Insert Length: 1140 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham High quality sequence stop: 213.

Location/Qualifiers

1. .460

//Organism="Homo sapiens"
//Organism="Homo sapiens"
//Clone="INAGE:1523481"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I to 460; NGT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NGT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                           221 TCAGGGACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 280
                                                                                                                          281 TGACAGCCATTGAAGCCTGTGTCCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAG 340
                                                                                                                                                                                                                                    AA909652 460 bp mRNA EST 10-JUN-1998 0114405.s1 Soares_KFL_TGGG_S1 Homo sapiens cDNA clone LMGE:1523481 3' similar to WP.F59B2.3 CE00231 N-ACETYL-GLUCOSAMINE-6-PHOSPHATE DEACETYLASE;, mRNA sequence.
161 TCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCT 220
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                                                                                                                                                                                                                                                                                                    341 GCAGGCCCGACCCTGTCTTCAGCAGGCCCCCACC 376
                                                                                                                                                                                                                                                                                                                                        287 GCAGCCTCCAGGGCCGACTCCATGCTGCAGCCTGCC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soares and M.
166 c
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161 TCCIATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCT 220

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125 CARGATGTAGGTGGGCCTGGACGTGAAGGGACTCGTCGACGACGCACGAAGTCTGCGTCACA 184
                                                                                                                                         281 TGACAGCCATTGAAGCCTGTGTCCTTGTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAG 340
                                                                                                                                                                  65 TCCTCTCAGCCGAGGTCCTTGTCACTGCCTAGCTGCGTCCGCCTGCCACCACCAGCTCACC 124
                                                 341 GCAGGCCCCGACCCTGTCTTCAGCAGGCCCCCACC 376
                                                                                                                                                                                                                                                                   245 GCAGCCTCCAGGGCCGACTCCATGCTGCAGCCTGCC 280
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Search completed: March 19, 2000, 08:56:41 Job time: 583 sec

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50: gb_p13:*

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nu	nucleic search, using sw model
Run on:	<pre>March 18, 2000, 19:58:50 ; Search time 360.16 Seconds (without alignments) -1972.773 Million cell updates/sec</pre>
Title: Perfect score: Sequence:	US-09-092-296-7_COPY_51_284 234 1 ATGGGGTCTGGGCTGCCCTACCATGTTGTCTGCAACACA 234
Scoring table:	IDENTITY_NUC
Searched:	821193 seqs, -1518192014 residues
Database :	GenEmb1:*
Word size :	0
Number of hits	that pass the threshold : 1642386 1: 90_bal:* 3: 90_bal:* 5: 90_pal:* 6: 90_pli:* 8: 90_pli:* 9: 90_pli:* 10: 90_pli:* 110: 90_pli:* 111: 90_pli:* 112: 90_pli:* 113: 90_pli:* 114: 90_pli:* 115: 90_pli:* 116: 90_pli:* 117: 90_pli:* 118: 90_pli:* 119: 90_

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ys - 1996 Compuden Ltd.		Pred. No. score gre and is de	is the numb sater than or erived by ana	er of equal lysis	Fred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.	d by chan the resu re distri	ce to have a lt being printed bution.	ત્વે
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CCCTACCATGTTGTCTGCAACACA 234		92.4	300	55	AP000511		AP000511 Homo sapi	Sapi
				11	AC004148		AC004148 Homo	sapi
			15.1	333	AC006329		AC006329 Homo	Sapi
192014 residues			14.3	4 4	AC012184		AC012184 Homo	sapi
				10	HS198C21		AL034400 Human	DNA
	0.0		14.	12	AC005090		AC005090 Homo	sapi
			14.0	100	AP000513		AP000513 Homo	Sapi
			14.0	11	AC004209		AC004209 Homo	Sapi
hold : 1642386			14.0	22	AC002327		AC002327 Mus m	nascu
				160	EHVI120824		295152 Romo sa	apien
			13.8	'n	PIGATA		J03021 Porcine	9
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	288		13.3	r 0	PTCABP ABO14540		X61915 P.thunbe	ergi
			13.2	11	AC003999		ACO03999 Humar	ad PAC
			13.2	Ξ:	CNSOIDTS		AL132857 Humar	chr
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			13.2	40	HSAPEVPL7		U72849 Homo sa	apien
			13.2		AC009152		AC009152 Homo	Sapi
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	2.04		13.2	~ &	SOYHKGPA ATAC006955		AC006955 Arabid	nyd dops
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	7 4 7		13.4	v <u>-</u>	ABU11114 RS265.714		ABULLI14 HOMO S	Sapi
	0 44	30.8	13.2 2141	121	AF073309		AF073309 Mus muscu	nosnu
			13.2				AC002399 Homo	sap1
					ALIGNMENTS			
	RESULT AB023048	н						
	LOCUS	×)23048 1926 no sapiens ge	50 bp nomic	AB023048 192650 bp DNA Homo sapiens genomic DNA, chromosome	PRI 6p21.3, H	PRI 20-NOV-1999 6p2l.3, HLA class I region,	on,
	ACCESSION		one:5319, com 023048	plete	sednence.			
	VERSION	_	AB023048.1 GI:5672603	56726()3			
	SOURCE	:	o sapiens ce	11_11	Bomo sapiens cell_line:978SK DNA, clone:53L9	ne:5319.		
	- Order		nomo saprens Eukaryota, Meta	zoa; (nomo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,	a; Verteb	rata; Mammalla;	
		ang ang	.heria; Pr1ma	tes; (atarrhini; Komin	idae; Hom	0	

AB023048 Homo sapi AP000511 Homo sapi AC005329 Homo sapi D86631 Mus sp. DNA AC012184 Homo sapi D86631 Was sp. DNA AC012184 Homo sapi AC005990 Homo sapi AC005990 Homo sapi AC002327 Mus muscu 255152 Homo sapi AC002327 Mus muscu U59812 Homo sapi AC002327 Mus muscu D3021 Porcine cho M2778 Fug choline AC00336 Homo sapi AC01594 Human DNA AC01552 Homo sapi AC01554 Homo sapi AC01595 Homo sapi AC01599 Human Chr CAC11399 Human Chr CAC11399 Human Chr CAC13347 Homo sapi AC0195 P. thunbergi AC0195 P. thunbergi AC0195 Homo sapi AC01109 Homo sapi AC011114 Homo sapi

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/standard_name="D6S1898"
/note="W1-9418;The location is between each flanking site
of PGR PLIMETS."
(Ab, xref="GDB:678272"
complement(115656.115896)
/note="GdaVhi0;The location is between each flanking site
     Japan Science and Technology Corporation (JST)
5-3, Yonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan
For further infomation about this sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
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/note="075233;The location is between each flanking site
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/standard_name="10652088"
/note="SHGC-12985;The location is between each flanking
alte of PCR primers."
/db_xee="GDB-735268"
115648. .115904
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Homo sapiens clone UWGC:370M23.002 from 6p21, complete sequence.
ACOOS937.1 GI:3845393
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(164525. .164665)
/note="SHGC-3064;The location is between each flanking
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47531 c 49366 g 50498 t
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                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of PCR primera."
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Saluta 7. and Taxiahima, N.

Shilina 7. and Taxiahima, N.

Direct Submission

L. Submission

Shilina, Toxia Intraversity School of Medicine, Department of
Molecular Life Science 2: Bohseddai, Isehara, Kanagawa 259-1193,
Japan (E-mail:tahiina@is.icc.u-tokai.ac.jp, Tel:@i-463-93-1121,

Fax:@i-463-94-880,

L. 192650

// Corganiam="Homo sapiens"

// Chromosome="E" taxon:9606"

// Chromosome="E" taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shifma, S., Tamiya, G., Oka, A. and Inoko, H.
Shifma, S., Tamiya, G., Oka, A. and Inoko, H.
Homo sapiens 2,229,819bp genomic DNA of 6p21.3 HiA class I region
Publiahed Only in Database (1999) In press
I (bases 1 to 200000)
Hizakaa, M., Yamaguchi H., Imai, K. and Shimada, J.
Direct Submission
Submitted (21-SEP-1999) to the Dubl/EMSE, Genbank databases. Mika
Hizakawa, Japan Science and Technology Corporation (JST), Advanced
Databases Department: 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
Japan (E-mail:mikaferoko-jat.go.jp,
UR::http://www.aiis.tokyo.jst.go.jp,
Fax:81-3-5214-8470)
This sequence is conducted by Tokai University as a JST sequencing
          A. Salues). Tamiya, G., Oka, A., Takishima, N., Yamagata, T.,
Kikkewa, E., Irata, K., Tomizawa, M., Okuaki, N., Wuwano, Y.,
Watanabe, X., Fukuami, Y., Itakura, S., Sugawara, C., Ono, A.,
Yamazaki, M., Tashiro, H., Ando, A., Ikemura, T., Soeda, E., Kimura, M.,
Bahram, S. and Inoko, H.

Mahram, S. and Inoko, H.

Mahram, S. and Toko, H.

Molecular dynanics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp MLA class I region

Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
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chromosome 6p21.3, HLA Class I region,
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Principal Investigator: Hidetoshi Inoko Ph.D
Principal -463-93-1121, Fax:+61-463-94-8884,
The sequence is submitted by Ruman Genome Sequencing in ALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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44743 c 45833 g 52212 t
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AP000511.1 GI:5926698
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insertion of 175p repeat"
11556 a 11489 c 12284 g 11994 t
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2. 37648

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6. .38700

_family="MER3"
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5. 33767
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j. ,34290
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/rpt_family="MER5"
43325
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This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
Happing at the sequence predicted fragments is given below
Small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.
                                                                                                                                      Large scale sequence analysis of the human WHC class I region pubblished (1998)

Fred Mutchinson Cancer Research Center
Fred Mutchinson Cancer Research Division

The Clinical Research Division

1100 Fairview Ave N. P. D. Box 19024

Seattle, WA 98109-1024

C Dasses I to 47323)

Direct Submitsion

L Submitted (05-007-1998) Human Genome Center

Submitted (05-007-1998) Human Genome Center

Ontact: Daniel E. Geraghty (geraghty@fhcrc.org)

Overlapping Sequences: Geraghty (geraghty@fhcrc.org)

S: UWGC:370m23.013 (Genbank Accession: AC005530)

3: UWGC:970-112 (Genbank Accession: AC004211)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Quality Assessment:
f) is entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
quality! levals above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 47323)
Janer, M., Guillaudeux, T., Vu, Q., Kutyavin, T., Harter, H. and
Geraghty, D. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HindIII Neil Seq Map Seq 889.55 866.00 30541.40 30653.00 1050.18 1015.00 3279.08 3231.00
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DS or two chemistry coverage: 98.9%
Single stranded regions: 3
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1. .47323
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           SOURCE
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195-384)*
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complement(20794. 20934)
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| complement(1553)
| / TPL family "Alusx" | 16126)
| complement(15844. . 16126)
| / TPL family "Alusx" | 17334
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ement(2002)
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complement(3402...3677)
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                                                                                                                                                             complement (295. .592)
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complement (1063. .1204)
/rpt_family="LIMB8"
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/rpt_family="(TAAAA)"
complement(2195. 2480)
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10312. 10478
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10508. 10530
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/rpt_family="(CA)n"
complement(1279. .14
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Burkaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalla;

Eutharia: Primates: Catarrhini; Hominidae; Homo.

Eutharia: Primates: Catarrhini; Hominidae; Homo.

1 (bases I to 118276)

Es Birren, B., Linfon, L., Nusbaum, C. and Lander, E.

Homo appiens chromosome I7, clone HGIT52465

Li Upublished

Dupublished

Burren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Cooke, P., Barnan, J., Depayre, E., Davon, K., Dewar, K., Donelan, J., Ocoke, P., Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cerny, J., Cooke, P., Boutwell, C., Byrne, E., Devon, K., Dewar, K., Donelan, L., Durette, B., Etemadi, S., Perreira, P., Forrest, C., Funke, R., Gage, D., Gardyna, S., Genseland, J., Marguis, N., McEwan, P., Mcdurk, A., Meldrim, J., Marguis, N., McEwan, P., McMill, L., Linfon, L., Mackenie, J., Marquis, N., McEwan, P., McMilley, R., Noberts, D., Parlins, G., Rossello, R., Roy, A., Shyam, R., Soohoo, S., C., Sydney, K., Tang, L., Vassello, R., Roy, A., Shyam, R., Scohoo, S., C., Sydney, K., Tang, L., Vasselliev, H., Wagner, A., McMiller, J., Muller, H., Wagner, A., Shyam, R., Scohoo, S., C., Sydney, K., Tang, L., Vasselliev, H., Wagner, A., McMiller, J., McMiller, H., Wagner, A., Shyam, R., Scholer, J., Muller, H., Cantever, L., Can
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Direct Submission

Submitted (16-FEB-1988) Whitehead Institute/MIT Center for Genome Submitted (16-FEB-1988) Whitehead Institute/MIT Center for Genome Submitted (16-FEB-1988) Whitehead Institute/MIT Center for Genome States, Job Charles Street, Cambridge, MA 02141, USA

S SITEM. J., Fasaman, K., Linton, L., Narbaum, C., Lander, E., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Colayer, C., Colains, S., Collymore, A., Cooke, P., Colains, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Garthas, D., Depayr, E., Forrest, C., Funke, R., Gage, D., Garthas, D., Depayr, E., Hagos, B., Haerbor, M., Herena, L., Horton, L., Howland, J.C., Macdonald, P., Marquis, M., McGur, J., Monla, M., Morris, W., Morrow, J., Mochand, J.C., Mochand, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Maddonald, P., Malfel, M., Morris, W., Morrow, J., Mychalecky, J., Pavilin, B., Peterson, K., Riber, M., Morrow, J., Mychalecky, J., Pavilin, B., Peterson, K., Ribell, J., Stolanovic, M., Stilvell, J., Stolanovic, M., S
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                                                                                         AC004148 118276 bp DNA PRI 28-AUG-1998 Homo sapiens chromosome 17, clone HCIT524C5, complete sequence. AC004148 AC01418 GI:3482960
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                      l; indels
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/db_xref="taxon:9606"
/clone="HCIT524C5"
                      Matches 93; Conservative
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Direct Submission
Submitted (109-2NN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis Mo 53108, USA.

On Mar 13, 1999 this sequence version replaced 91:4138779.

* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigns. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigns are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
DD 68691 AACTGTGGCCATGTTTTTTTTTTTTTAAAGACCAGTGTGATAGTAGGCCATGCA 68634
                                                                                                                                                                                                                                                                 ACO06329 207984 bp DNA HTG 13-MAR-1999

Homo sapiens clone NH0132A01, *** SEQUENCING IN PROGRESS ***,
unordezed pieces.
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;
Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 207984)
Waterston, R.H.
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/organism="Homo saplens"
/db_xref="Laxon:9606"
/clone="NH0132A01"
53798 a 51576 c 52041 g 50425 t
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Inpublished
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6134
                                                                                                                                                                                                                                                                    .complement(20970. .21272)
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:omplement(21467. .21955)
/rpt_familv="To"
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lement(27381. 27601)
family="Tigger1"
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ppt_family="LiM4"
pmplement(25404. .25427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              omplement(25428. .25741)
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omplement(25742. .25828)
rpt_family="L1"
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rpt_family~"AluJb"
omplement(30527. .30597)
rpt_family~"LIMA2"
30735
                                                                                                                     t(21966. .22276)
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7. .2480
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rpt_family="Aluxa8"
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pt_family="Tigger1"
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lement(30207. .30260)
family="LLMA2"
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complement(22808. .22989)
rpt_family="MER46A"
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/rpt_femily="Alusp"
28938. .28966
/rpt_femily="Ar_rich"
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pt_family-"ar_rich"
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complement(23760. .24
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0736. .31042
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/rpt_family="A
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22 C [bases I to 65673)

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No Submitted (21-COT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA www.jg.i.doe.gov.

* WOTE: This is a "working draft, sequence. It currently consists of 40 contigs. The true order of the pieces is no frown and their order in this sequence record is a thin story agas between the contigs are represented as a round of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 16 clone RPCI-11_529K1, *** SEQUENCING IN PROCESSS ***, 40 unordered pleces.
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1 (bases 1 to 65673)

10 Dou Johnt Genome Institute.

Sequencing of Human Chromosome 16

Oppublished
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                                                                       Query Match
14.6%; Score 34.2; DB 12; Length 3626;
Best Local Similarity 60.0%; Pred. No. 2.8;
Matches 57; Conservative 0; Mismatches 38; Indels 0;
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10N Mus sp. DNA for oxytocin receptor, partial cds.
1086631.1 GI:1902965
10 Sytocin receptor.
11 Oxytocin receptor.
12 Nus sp. (strain:1295V) ES cell DNA.
13 Mus sp. (strain:1295V) ES cell DNA.
14 Sp. Sciurognathi, Muridae; Murinae; Mus.
15 Chaes 1 to 3626)
16 Chaes 1 to 3626)
17 Chaes 1 to 3626)
18 Submitsaton
19 Sibmitted (26-JUL-1996) to the DDBJ/EMBL/GenBank databases. Yasue Rubota. Osaka University Medical School, Department of Obstetrics and Gypeoclogy; 2-2 Ramadaoka, Suita, Osaka 565, Japan (E-mail:kubota@gyne.med.osaka-u.ac.jp, Tel:81-6-879-3351,
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                                                                             174 TTCAGGGACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACAC 233
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Rubota Y., Kimura Y., Hashimoto, K., Tokugawa, Y., Nobunaga, K., Azuma C., Sqil.F. and Murata, Y.

Structure and Expression of the Mouse Oxytocin Receptor Gene Unpublished (1996)

3 (sites)

Rubota Y., Kimura Y., Hashimoto, K., Tokugawa, Y., Nobunaga, K., Azuma C., Sqil.F. and Murata, Y.

Structure and expression of the mouse oxytocin receptor gene Moi. Call. Endocrinol. 124 (1-2), 25-32 (1996)
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/strain="1295V"
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Reach, P.

Direct Submission

AL Submitted (16-MAR-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1834, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: cionerequest@sanger.ac.uk
cB10 1834, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: cionerequest@sanger.ac.uk
on Mar 21, 1999 this sequence version replaced g1:3980345.

During sequence assembly data is compared from overlapping clones
where differences are found these are annotated as variations.
Where differences are found these are annotated as variations corresponding to the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
IMPORTANT: This sequence is not the entire insert of clone 198021.
If may be shorter because we arrange for a small overlap between
neighbouring submissions.
The true right end of clone d335887 is at i00 in this sequence.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e-g. Alu). Where the
sequence was generated from part of bacterial clone contigs of
human chromosome X, constructed by the Sanger Centre Chromosome X
http://www.sanger.ac.uk/GBV/ChrX
198021 is from the library RPCI6 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://Acapac.med.buffaio.edu/ vECTOR: pPAC4.

1 LA1762 and the data of the d
                                                                                                                                                                                                             HS198C21 141762 bp DNA PRI 23-NOV-1999 MIMMAN DNA sequence from clone 198C21 on chromosome Xq26.1-26.3 Contains GPC4 (q1ypican 4), ESTs, STSs and GSS, complete sequence. AL0314400
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| . . 397
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/57. 810
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     Db 39755 TANACTICANAGCGCANATICCIGIGAIGCA 39725

    141762
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    /db_xref="taxon:9606"

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
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note-"AluJo/FLAM repeat: matches 1. .133 of consensus"
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/note="11PB3 repeat: matches 6035. .6147 of consensus"
1446. 14489
/note="11 copies 4 mer gaat 77% conserved"
14629. 14920
/hote="AluJo repeat: matches 1. .291 of consensus"
14971. 15016
/note="12 repeat: matches 2651. .2696 of consensus"
15708. 16063
/note="12 repeat: matches 1. .362 of consensus"
15708. 16063
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28044. .28342
/note-"Alusx repeat: matches 258. .515 of consensus"
/note-"Alusx repeat: matches 1. .299 of consensus"
28575 .28770
                                                                                                                                                                                                                                                                                                                       4972. 5123

//Octe-*Alusx repeat: matches 126. .287 of consensus*

//Octe-*Alusx repeat: matches 1. .296 of consensus*

//Octe-*Alux repeat: matches 1. .296 of consensus*

//Octe-*Alux repeat: matches 1. .126 of consensus*

//Octe-*Alux repeat: matches 1. .126 of consensus*

//Octe-*Alux repeat: matches 3. .324 of consensus*

//Octe-*Alux repeat: matches 3. .324 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8348. .8438

Mote-*L2 repest: matches 2598. .2700 of consensus*

Mote-*L2 repest: matches 2598. .2700 of consensus*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 repeat: matches 2588. .2710 of consensus.
10378
                                                                                                                                                      3303. 3435.

7hote-"FLMA repeat: matches 1. .133 of consensus"

7hote-"16 coples 2 mer aa 91% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      occe-Aluss repeat: matches 1. .299 of consensus 0383. .10517 repeat: matches 1. .142 of consensus note-Alubb repeat: matches 1. .142 of consensus 0570. .10796
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note="10 copies 3 mer tga 97% conserved"
4595. .24894
note="Alluo repeat: matches 1. .286 of consensus"
4998. .25029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alusx repeat: matches 1. .297 of consensus"
.26990
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Note-"MERSA repeat: matches 9. .112 of consensus"
                                                                                                                                                                                                                                                                               851. 4963
note="SVA repeat: matches 764. .870 of consensus"
                                          498. . 1/82
note-"Alusg repeat: matches 1, .293 of consensus"
                                                                                  2804. .3085
Anote-'3106
3091. .3126
Anote-"9 copies 4 mer aata 83% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16648. 16836 Traces 9. .112 of consensus' note-"MIR repeat: matches 47. .237 of consensus" (8665. .17136
2263. .2496
/note="MIR repeat: matches 20. .262 of consensus"
                                                                                                                                                                                                                                    734. 4771
/note-19 copies 2 mer tt 79% conserved
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                                                                                /note-"MER5A repeat: matches 1. .154 of consensus"
28879. .29178
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RESULT 9
AC005090/c
LOCUS
DEFINITION
ACCESSION

ORGANISM

VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE JOURNAL

AUTHORS TITLE

JOURNAL

REFERENCE

AUTHORS TITLE JOURNAL

REFERENCE

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18790
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Submitted (27-AUG-1998) Department of Genetics, Washington
Submitted (27-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
ON Aug 27, 1998 this sequence version replaced gi:3212901.
SUBMITTED BY: WUGSC
Genome Sequencing Center
Department of Genetics
Mashington University
St. Louis MO 63108, UGA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Mashington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (12-UN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone RG31510 is from a release of the human BAC library CTTB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1995). The clone is available from VECTOR: pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
ACO05090 116218 bp DNA PRI 27-AUG-1998
Homo sapiens BAC clone RG315L10 from 7p14-p15, complete sequence.
ACO05090
                                                                                                                                      Homo saplens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 116218)
Dauphin, S. and Biewald, T.
The Sequence of Homo Sapiens BAC clone RG315L10
Upublished (1998)
2 (bases 1 to 116218)
Waterston, R. H.
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                                                                       AC005090.1 GI:3478661
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Waterston, R.
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                                                                                                                        human.
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repeat_region

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26886. .27047 /rpt_family="MIR" 27462. .27574

repeat_region

repeat_region

The actual start of this clone is at base position 1 of RG315L10; actual end is at 116218 of RG315L10.

NEIGHBORING SEQUENCE INFORMATION:

Bases 41827 to 41835 of this sequence are single stranded. Base 41828 is of low quality and could be a G or an A. Location/Qualifiers

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1 (sites)
Shina.T., Tamiya.G., Oka.A., Takishima.N., Yamagata,T.,
Kikkawa.E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
Watanabe.K., Fukuzumi,Y., Itakura.S., Sugawara,C., Ono,A.,
Watanabe.K., Tashiro.H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahram.S. and Inoko.H.,
Molecular dynamics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp HLA class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
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AP000513.1 GI:5926700
                                                                                                                                                                                                    Homo aapiens (haplotype:HLA-DR4) adult male blood Immunoresponse
cell cell_line:Boleth DNA, clone_lib:CEPH YAC clone:745b12 and
                                         AB014077 30452 bp DNA PRI 20-NOV-1999 Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region, cosmid clos:IY7H8, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 CCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAG 123
                                                                                                                                                                                                                                                                                                        Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. Similarity 58.0%; Pred. No. 8.5;
58; Conservative 0; Mismatches 42; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organiam="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="blood"
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6763 c 7522 g 8435
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AB014077.1 GI:5672586
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Best Local Similarity
Matches 58; Conserv
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APO00513/c
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ORIGIN
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           RESULT 10
ABO14077/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 CITIGCAACTGAAGGAGTCITITCTGACAAATTCCTCCTATGAGTCCAGCITCC 133
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Pred. No. 8;
0; Mismatches 75; Indels 0;
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complement(31189. .31236)
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31627. .31721
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31855. .31927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22865.32584

72pt_fanily"L2"

32740.33139

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33315.33521

7rpt_family"Alu"

33622.33745
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3619. 3644.3

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30119 307
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Best Local Similarity 51.0%;
Matches 78; Conservative (
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Direct Submission
Direct Submission
Submitted (03-5EP-1998) Human Genome Center, University of
Washington, Box 322145, Seattle, WA 98195, Seattle, WA 98195, USA
Fred Hutchinson Cancer Research Center
The Clinical Research Division
                                                                                                                                                                                                                                                                                                                Db 91709 CCGCCCCTCTCACCACCTCCAGCATCCTACTCTAAGCAACTCTTATTCTCT 91650
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This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
quality, levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                   64 CCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Large scale sequence analysis of the human MHC class I region Unpublished (1998)
Fred Witchinson Cancer Research Center The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
2 (Dasse I to 4360)
Geraphy, D.B. and Olson, M.V.
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This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACO04209 43600 bp DNA PRI 03-SEP-1998 Homo sapiens clone UNGC:y55c025 from 6p21, complete sequence. ACO04209.1 GI:3522963
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 43600)
Janer,M., Guillaudeux,T., Vu,Q., Kutyavin,T., Harter,H. and
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                                                                                    Query Match 14.0%; Score 32.8; DB 10; Length 100000; Best Local Similarity 58.0%; Pred. No. 9.1; Matches 58; Conservative 0; Mismatches 42; Indels 0; (
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Seattle, MA 98109-1024
Contact: Daniel E. Geraghty (geraghty@fhoro.org)
on Sep 3, 1998 this sequence version replaced gi:2905851.
Overlapping Sequences:
5, 10MGC:y55c174
3': UMGC:y55c068
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Submitted (23-FEB-1998) Human Genome Center, Un
Mashington, Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 4360)
Geraghty, D. E. and Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Oy 124 TCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTC 163

Db 91649 CCTAGATTACTGAAATTGCCTCACACTCTCTGTGCTCC 163
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DS or two chemistry coverage:
Single stranded regions:
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Phone: 481-463-93-1121, Faz: 481-465-94-8884,
Project of JST
Japan Science and Technology Corporation (JST)
Japan Science and Technology Corporation (JST)
For further infomation about this sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or eand email to webmaster@www.alis.tokyo.jst.go.jp.
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complement(25387. 25469)
/note="1516/31567.The location is between each flanking site of PGR primers."
db_xref="60381515649"
complement(36020. 36562)
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//nore="1885/2186;The location is between each flanking
site of PCR primers."
                                  Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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23716 c 23917 g 26637 t
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    Homo saptens DNA.
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/rpt_family="Alu" repeat_region complement(2797628261)	/rpt_ramly="Alu" repeat_region complement(2839428664) /rpt family="Alu"	repeat_region 28716. 28998	repeat_region confit. (2974 29952)	repeat_region complement(30110, .30353)	<pre>/rpt_tamily="Alu" repeat_region complement(3045130660)</pre>					/rpt_family="MER42		3211232243 /rpt_family="Alu"			repeat_region 33680339/l	repeat_region 3433134939 /rot_family="Alu"	repeat_region 3520035499	repeat_region 35190 (25190)	repeat_region complement(3637736494)	/rpt_tamily="LTR8" repeat_region 36578 36830	/rpt_family="Alu" repeat_region 3701137330	/rpt_family="Alu" /rpt_family="Alu" /rpt_fament(3753037676)		/rpt_family-"Alu" complement(38785.	/rpt_family="Alu"	/rpt_family="Alu"	/rpt_family="Alu"	region complement(4060)43600)	BASE COUNT 11071 a 9661 c 10338 g 12530 t ORIGIN		0%; Score 32.8; DB 11; Length 43600; 0%; Pred. No. 8.7;	drive of mismaccies 42; inders of caps		Db 17165 CCGGCCCTGTCTCACCTCCAGCTCCAGCTCCTACTCTAAGCAACTCTTATTTCTCT 1/106	Oy 124 TCCAGCTTCCTGGAATTGCTTGAAAGCTCTGCCTCCTCC 163	Db 17105 CCIAGATIACTGAAAIAGCCICAACTGTCTCTGTTCC 17000	RESULT 13
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f (approximately 400-600bp) in the table. There are no	tween the experime gment groups are s	NS11	č	٠.	1	8400.84 8055.00	10629.14 10329.00	951.62 941.00	763																												
Small fragments below a variable cutoff (app are not mapped and hence do not appear in th	epancies be ordered fra	Hindiii		1347.00	1360,00	1799.00	12685.00	4138.00	727.00			8204.00	7605.00	•	" sub-	96	12"	/sub_cione= owc:ysscozs /cell_line="CGM1"	IAC LIDIALY	<u>-</u>		.1448)		.2913)	.6708)	.7129)	.7543)	(0777.	.8535)	(0606)				.19743)	.26590)	.27017)	(36772.
below a var nd hence do	tining discr . Uniquely	Hir	400	•	_ '	20 1803.37	13189.91	00 4298.12	736.47	28	٠	00 8505.16	7741.77	. ag	143600 /organism#"Homo saniens	/db_xref="taxon:9606" /chromosome="6"	CGM1: D123C	ne CGM1	11D - Wash U	complement(21277) /rpt_family="Alu"	73 111y="Alu"	<pre>complement(11501 /rpt_family="Alu"</pre>	2345 111v="Alu"	complement(2630	ant (6636.	complement (6854.	complement (7265.	nily="Alu" ent(7635	/rpt_family="L1" complement(8253	/rpt_family="Alu" complement(8973:	/rpt_family="Alu" 1550715767	/rpt_ramily="Aiu" 1752817816	/rpt_family="Alu" 1835418646	mily="Alu" ent(19460.	/rpt_family-"Alu" complement(26422.	/rpt_family="MER42" complement(2672227017)	/rpt_family="Alu" complement(27496.
fragments t mapped a	icant rema ted values hed lines.	Bglii	- :	•	7:	.61 627.00	85 11969.00	25 8932.00	86 2596.00			9		Location	143600	/db_xred	/clone=	/cell_li	/map="6p21"	<pre>complement(21. /rpt_family="A]</pre>	67687 /rpt_fam	compleme /rpt_fan	2056	compleme	compleme	complem	compleme	/rpt_far	/rpt_far	/rpt_far	/rpt_far 15507.	/rpt_far 17528.	/rpt_far 18354.	/rpt_far	/rpt_far	/rpt_far	/rpt_ran
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.y="AluSq/x"

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4603 .4679

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/rpt_family="MERSA"
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Complement(9699. .9812)
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24457..24544
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9549, .19601
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rpt_family="Alusp"
806. .2832
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765. .14811
                                                                                                                       /rpt_family="(A)n"
2852. .2914
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Submitsed (15-701-1997) Whitehead Institute/MIT Center for Genome Submitted (15-701-1997) Whitehead Institute/MIT Center for Genome Research 320 Charles Street, Cambridge, MA 02141, USA Bitren, 2. Inton.L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Castle,A., Cerny,J., Colangelo,M., Beckerly,R., Benn,J., Brown,A., Cooke,P., DeArellann,K., Depayre,E., Devon,K., Dewar,K., Funke,R., Gage,D., Galagan,J., Gardyn,S., Gilbert,D., Grant,G., Rartas,A., Henford,A., Horton,L., Howland,J.C., Jones,C., Kan,L., Martas,A., Lehoczky,J., Lieu,C., Looke,K., Wacdonald,P., Martas,A., Lehoczky,J., Lieu,C., Looke,K., Wacdonald,P., Martas,A., McDran,P., McReman,K., McDauphlin,J., Naylor,J., Niloff,M., Worls,W., Wacrens,K., McCangli,P., Pattlin,B., Stange-Thoman,W., Stojanovic,N., Vossillov,H., Vo,A., Ragner,A., Direct Submission

Naylor,J., Wu,K., Wyman,D., Ye,W.J. and Zody,M.

Submitted (102-FEB-1999) Whitehead Institute/MIT Center for Genome On Feb 2, 1999 this sequence version replaced di:4204708.

Green, P., 1995-1997) fited using RepeatMasker: Smit, A.F.A., a http://frp.genome.washingted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Research Genetics/Cal Tech CITB9785K-B (plates
                                                                                                                                                                                                                                                                 Hawkins,T.L., Reeve.M.P., Christoffersen,A., Birren,B.W.,
Barna,N.H., Lander,E.S., McKernan,K., Munco,C., Richardson,P.,
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McDermott,J., Mollan, Lee,R., MacKenzie,J., Marquis,N.,
Maylor,J., O'Connor,T., Olotu,A., Peterson,K., Rollins,G.,
Traish,A., Wilmer,F., Zemtseva,I. and Zody,M.C., Sydney,K.,
Sibmission
        AC002327 159515 bp DNA ROD 02-FEB-1999
Mus musculus chromosome 7, clone 19K5, complete sequence.
                                                                                                                                 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 7, clone 1985
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Litter Submitted (02-APR-1998) Chromosome 6 Project Group (http://wwwsanger.ac.uk/RGP/Chr6/) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquires:

Cambridgeshire, ac.uk/GD/Chr6/) Sanger Centre, Hinxton, Cambridgeshire, ac.uk Clone requests: clonerequest(Sanger.ac.uk Clone ac.uk Clone is the entire insert of clone 179N16.

IMPORTANT: This sequence is the entire insert of clone 179N16.

IMPORTANT: This sequence is the compared from overlapping clone invariations where differences are found these are annotated as variations coperated may not be found in the sequence submits sequence submits only a small overlap as described above.

This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed in collaboration by the Sanger clettre chromosome 6, constructed in collaboration by the Sanger information can be found at http://www.sanger.ac.uk/RGP/Chr6/ This sequence has been finished according to sequence map criteria as follows. An attential and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is amontated human repeat sequence elements (e.g. Alu). Where the man annotation using the 'unsure' man annotation using the 'unsure' man annotation and annotation whose mander and annotation whose mander and annotation whose mander and annotation using the 'unsure' mander and annotation using the 'man annotation whose mander and annotation whose mander and annotation whose mander and annotation where the mander and annotation using the 'mander and annotation whose mander and annotation whose mander and annotation where the mander and annotation where the mander and annotation whose mander and annotation where the mander and annotation where the mander and annotation when the whose mander and annotation when the mander and annotation when the ma
                                                    HS179N16 172048 bp DNA HOMO Sapient 23-NOV-1999 Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (NAPK p386atle) gene, and the alternatively spliced SAPK4 ene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTS, STSs and two predicted CPG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The true left end of clone 179N16 is at 1 in this sequence. The true right end of clone 524E15 is at 690.

The true left end of clone 179N16 is at 172048.

The true left end of clone 179N16 is at 172048.

TOWNE is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see http://bacpac.med.buffalo.edu/.

1. 172048.
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/note-lanna repeat: matches 324 . 574 of consensus"

1565. 2257

/note-"Alujb repeat: matches 1. 302 of consensus"

228. 2543

2404. 1214B6 repeat: matches 566 . 874 of consensus"

2548. 2848
                                                                                                                                                                                                                      295152.1 GI:3036773
HTG; CpG igland; CSaids binding protein; CSBP2; MAPK; Mitogen
activated protein kinase; MXI2; P38; SAPK4; Stress activated
protein kinase
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172048)
Palmer S.
Direct Submission
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193. .734
/note="Alujo repeat: matches 302. .62 of consensus;
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14.0%; Score 32.8; DB 12; Length 159515;
Best Local Similarity 53.0%; Pred. No. 9.4;
Matches 70; Conservative 0; Mismatches 62; Indels 0;
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complement(30322. 30465)
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complement(27608. 27662)
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complement(25541, .25624)
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50929, .50965
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43715. .43742
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incomplete repeat."
21094. 21432
//note-"MEXLB repeat: matches 1. .337 of consensus."
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22054. .22225 //note-"AluJb repeat: matches 131. .301 of consensus; incomplete repeat: matches 131. .301 of consensus; //note-ment(22217. .22628)
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Afonce="match: cDNAs U93232 U66243 Y10487 AF015256 Y10488
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27782. .27861,29276. .29347,29456. .29570,29695. .29742,
30178. .30207,30365. .30473,33547. .33605,34826. .34955,
35255. .35643)
/gene="SAPK4"
                                                                                                                                                                                                                                                                                                /evidence-not_experimental
/product="dJ179N16.1 (Stress Activated Protein Kinase 4
(Mittogen Activated Protein Kinase p38delta))"
complement(26546. .35905)
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/evidence-not_experimental
/product-dall9N16.1 (stress Activated Protein Kinase
/Mitogen Activated Protein Kinase p38delta))*
/protein_id="CAB08438.1"
/db_xref="GI:3036774"
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/codon_start=1
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Matches 62;
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13595. 13953

/note="IHEIB repeat: matches 364. 1 of consensus"
1372. 14648

/note="11MC3 repeat: matches 1676. 2345 of consensus"
/note="11MC3 repeat: matches 1. 301 of consensus"
/note="11MC3 repeat: matches 1. 301 of consensus"
/note="11MC3 repeat: matches 2336. 2470 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15102. 15331
/ Onche"FLAM, A repeat: matches 133. .4 of consensus"
15244. 15283
/ Inche"FLAM, Separat: matches 133. .4 of consensus"
15244. 15853
/ Inche"match: Z63849 Cpc Island clone 91c11"
/ Inche"matches 33. .394 of consensus"
/ Inche"matches 4. .151 of consensus"
/ Inche"matches 4. .151 of consensus"
3168. .3369
/note="MER44C repeat: matches 258. .463 of consensus"
                                                                                                              5473. .8894
//note="WLTIC repeat: matches 39. .465 of consensus" 5986. .6284
//note="Alub repeat: matches 1. .296 of consensus" 6361. .6420
//note="Alusx repeat: matches 301. .242 of consensus" //note="Alusx repeat: matches 301. .242 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7977. .18027
note="MLT2FA repeat: matches 400. .450 of consensus"
                                                                                                                                                                                                                                                                                                                                     6612. .6914 // Mote #AluJb repeat: matches 2. .302 of consensus # 6951. .7084 // Mote #ELAM_C repeat: matches 1. .133 of consensus # / Mote # FLAM_C repeat: matches 1. .133 of consensus # / Mote # FLAM_C repeat: matches 1. .133 of consensus # / Mote # / M
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13494. .13581
Anote-"AluSx repeat: matches 205. .288 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 5068. .5387 of consensus"
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note "LIMC2 repeat: matches 15. .384 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8605. 8691
/note="MER2 repeat: matches 125. .209 of consensus"
8826. 8890
/note="MER2 repeat: matches 279. .344 of consensus"
                                                                                   note="AluJb repeat: matches 289. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8396. .8603
/hote="AluJb repeat: matches 291. .82 of consensus;
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'note="MERLIB repeat: matches 2. .627 of consensus"
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te="MER2 repeat: matches 13. .136 of consensus"
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//note="Alusg repeat: matches 300. .1 of consensus" 12207. 11233
//note="Min repeat: matches 106. .248 of consensus" 12735. .13031
//note="Alusx repeat: matches 1. .298 of consensus" 13042. .13256
//note="Alusx repeat: matches 2. .217 of consensus" //note="Alusy repeat: matches 2. .217 of consensus;
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Anote="AluJo repeat: matches 85. .301 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9518. 9894
/note="THELC repeat: matches 3. .371 of consensus" 9964. 9989
10964-13 copies of 2 mer 96 % conserved" 10970. .11269
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Pysdpylgypfbelikhilgadaraagragggreaamlprogesylshlaavngyhyk
gdgaalrylfsslsvlaghtfesebgrlabisnlyytwssradbggydaratsss
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LTTEEALLAWLVDECKEYLHOLIELWMQVPVSYDAPTTSAINNSLGIIRQTHGGGED
NFGRLLCSLSFASCETLELVLQSDERCLSVFASELAKFYVESQNLWLAYSGGLSAGLRE
RFPRSWLYFALKQKWLRFIYFFK"
Anote="QRF G6"
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29997. .32183
/note="ORF 07"
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/product-"tegument protein"
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/db_xref-"GI:695176"
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/function="role in capsid
/protein_id="AAC13794.1"
/db_xref="G1:695179"
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/db_xref="G1:695177"
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/note="ORF E4"
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/ CRANTAMALLANDAYDESAPCKSDTTMAAQVY PALTLIAFEGLGGNILVITVITVNTKITRMK
IKNLTNMLLLNAISDLIELLTIPFWARTALTSAQVY PARTLIAFGLSCKLLGGVCYMSLYSOV
FOITILLYDRYLLAVYAVTALLERFTYTGGIVTCVCTWFLAGLLSLPEFFHGHQDDNG
RVQCDPYYPBKSTNVWRRAHVARVIMLSLILPLLIAMQCTYVIIRRLERFBSKKKYR
IRLIFWNAYRYFRHHYMPFHTYVALLSTFHATLMIQCALSSNLDMALLITKTVAYTHCC
IRVYIXARVGEFFRHHYMPFHTYVALLSTFHATLMIQCALSSNLDMALLITKTVAYTHCC
10494. . 10499
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TLMPTSTSTTTPVTTGIFPDPQNTTHPTHFTVKPTRRPINLLREGYTPWALITLVVIIL
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Note-FORE E2.
19784. .19789

/note-FORE E2.
/note-FORE E3.
20320. .2084

/note-FORE E3.
product has N- and C- hydrophobic domains and 6 N-linked glycosylation sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (09-FEB-1995) Elizabeth A.R. Telford, Institute of
Virology, MRC Virology Unit, University of Glasgow, Church Street,
Glasgow Gll 5JR, United Kingdom
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                         Betaherpesvirinae.

1 (bases 1 to 184427)

Telford, E.A., Watson, M.S., Aird, H.C., Perry, J. and Davison, A.J.
The DNA sequence of equine herpesvirus 2
J. Mol. Biol. 249 (3), 520-528 (1995)
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/note="ORF E2; product has hydrophobic N-terminus"
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/protein_id-"AAC13788.1"
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/organism="Equine herpesvirus 2"
/strain="86/67"
                              Equine herpesvirus 2, complete genome.
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/note-"QRF 03"
/codon_start-1
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/note="ORF El"
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10660. 10665
/note-"ORF E1"
12533. 13114
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Telford, E.A.R.
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ö 0; Gaps DB 16; Length 184427; 91; Indels Query Match 13.8%; Score 32.4; DB Best Local Similarity 48.9%; Pred. No. 13: Matches 87; Conservative 0; Mismatches

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86816 GGTTCGGCTCCTGCGGATGACCTGGTTCTCCCCCACGAAGCCCTCCTACGAGGCCCATCCA 86757 72 GACTITGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGCTT 131 g

132 CCIGGAATIGCIIGAAAAGCICIGCCICCICCICCAICICCCIICAGGGACCAGGGIC 189 ö

Search completed: March 18, 2000, 20:18:44

Job time: 1194 sec

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

March 20, 2000, 09:13:57 ; Search time 76.27 Seconds
(without alignments)
767.601 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-092-296-7_COPY_51_284
234
1 AIGGGGTCIGGGCTGCCCCT......ACCAIGTIGTCTGCAACACA 234

IDENTITY_NUC Scoring table:

311585 seqs, 125096042 residues Searched:

N_Geneseq_36:* Database :

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623170 Number of hits that pass the threshold : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Score Match Length DB ID 234 100.0 237 100.0 238 12.8 23.8 23.8 12.8 23.9 12.8 23.9 12.8 23.9 12.8 23.9 12.8 23.9 12.9 23.9 12.9 23.9 12.9 23.9 12.9 23.9 12.9 23.9 12.9 23.9 12.9 23.9 12.9 23.9 12.0 23.9 13.0 24.9 13.0 25 | Ouery Score Match Length DB ID 234 100.0 439 1 V84366 30 12.8 1824 1 074052 31 12.8 14690 1 X22303 Human interleuki 29.8 12.7 291 1 V86365 EST clone AR34-1 274293 Human interleuki 29.8 12.7 291 1 V86365 EST clone AR34-1 12.6 6175 1 734291 EST clone Z386102 eST cl | Score Match Length DB ID 234 100.0 310.1 324 100.0 329 12.8 329.4 329.4 329.4 329.4 329.4 329.4 329.4 329.4 329.4 329.4 329.4 329.4 329.4 329.4 329.4 329.4 329.4 320.5 | Score Match Length DB ID 234 100.0 237 100.0 238 100.0 239 1 V84366 Human stomach can go 12.8 22.8 12.0 23.9 1 V85365 23.9 12.8 23.1 10.0 24.1 10.0 25.1 1 | Score Match Length DB ID 234 100.0 439 1 V84366 Human stomach can be a secretary can b | Score Match Length DB ID 24 100.0 24 100.0 26 12.8 27 100.0 28 12.8 29 12.8 29 12.8 29 12.9 29 12.9 29 12.9 29 12.0 29 12.0 29 12.0 29 12.0 29 12.0 29 12.0 29 12.0 20 12.0 2 |

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181 ACCAGGETCACCCTCCACCATGCAAGATCTCAACACCATGTIGTCTGCAACACA 234

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Ñ	one HP10408. human; stomach cancer; ds. lers prising the coding region (minus p codon) is claimed (Claim 3) " ansmembrane domains and their the preparation of antibodies and gene diagnosis, and gene therapy of cons. Islaimed) for a novel human is a signal sequence detection if a signal sequence and a putative is by in vitro translation. The invention provides nucleotide if on it is by in vitro translation. The invention provides nucleotide if on it is by in vitro translation. The invention provides nucleotide if on it is by in vitro translation of rich is transmembrane proteins and sections. The proteins can be cons in the preparation of ilgands corresponding to screening of low mol. wt. medicines or 234: In it is in the preparation of the preparation of ilgands corresponding to screening of low mol. wt. medicines or 234: In it is in the preparation of ilgands corresponding to screening of low mol. wt. medicines	Pred. No. 1.5e-64; Mismatches 0;
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ω ω ω ω ω	11. 1 1866 standard; CDNA 184366; 30.WAR-1999 (first en Human stomach carcinom Transmembrane protein); Homo sapiens. Evy 10.DEC-1998. 10DEC-1998; 10UNN-1997; JP-144948 (PROT-) PROTEGENE INC. (SAGA) SAGAMI CHEM RE: WALO S, SSKIME S, Yamag WALO S, YAMAG	Similarity 4; Conserv
22222	standard; 1999 (fit) tomach can blens. In 1988, J024 1998, J0	덛
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human II-Ira BAC contiguous DNA sequence 96.

Tango-77; human: II-Ira: cytckine superfamily; inflammation; inhibition; interleukin-1 receptor; II-IR; requilation; asthma; rheumatoid arthritis; chronic myelogenous leukeamia; psoriasis; inflammatory bowel disease; growth factors; treatment; II-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5839 ACICTACAGCIGGAGGTAAGTGAATGCIATGGAATGAAGCCCTTCTCAGCCTCCTGCTAC 5898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 ACTITGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTC 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 18; Page 17-20; 35pp; Japanese.

Example 18: Page 17-20; 35pp; Japanese.

074052 is interleukin-1-beta cDNA and 074019-21 are primers used for the amplification of this cDNA. They are used specifically for the detection and isolation of this sequence. The primers have the advantage of high sensitivity and reliability and are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A primer for the detection and the determn. of a specific messenger RNa - can detect and determine specific mRNA(s) with high
                                                                                                                                                                                                                                 29-JAN-1996 (first entry)
Human interleukin-1-beta.
Interleukin 1 beta; primer; mRNA: specificity; pharmaceutical; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2195 T;
12.8%; Score 30; DB 1; Length 7824;
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0; Mismatches
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03-AUG-1998; U16102.
02-AUG-1998; US-091650.
04-AUG-1997; US-054646.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                           /*tag- a /note- "N is undefined"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                            Q74052 standard; DNA; 7824 BP.
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05-NOV-1993; 275852.
05-NOV-1993: JP-275852.
(HITB) HITACHI CHEM CO LID.
WPI; 95-211627/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 55.9
Matches 57; Conservative
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WO9906426-Al.
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member of the cytokine superfamily that is expected to inhibit inflammation by binding to the interleukin-1 receptor (II-1R). It may also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic myelogenous leukemia, rheumatiod atthifts, psoriasis and inflammatory bowel disease. It may also induce or suppress interleukins, cytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex. 3810 A; 3245 C; 3299 G; 4327 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4343 ACTCTACAGCTGGAGGTAAGTGAATGCTATGGAATGAAGCCTTCTCAGCCTCCTGCTAC 4284
                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 ACTITGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGCTTC 132
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                                                                                                                                                                                                                                                                                                                                              DB 1; Length 14690;
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Local Similarity 70.2%; Pred. No. 1.9;
hes 40; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-APR-1998, U06954.
10-APR-1997; US-835913.
(GENY) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
Racie La, Spaulding Y, Treacy M;
WPI: 99-070076/06.
                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 7;
0; Mismatches 45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4283 CACTIAITCCCAGACAACCACCTTCTCCCCGCCCCATCCT 4242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 CTGGAATTGCTTGAAAGCTCTGCCTCCTCCTCCATCTCCCT 174
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                                                                                                                                                                                                                                                                                                                                                       12.8%; Score 30; 55.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 C;
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V86365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-APR-1999 (first entry)
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Best Local Similarity 55.99
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WO9845435-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-0CT-1998.
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Matches
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21-AUG-1985, JP-183810.
(SCHE ) SCHERING BIOTECH CO.
WPI; 87-097765/14.
             US-063595.
US-044428.
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21-AUG-1985; 183810.
                                                                                                                                                     WPI; 99-009434
P-PSDB; W89247
                              28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P7041
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                                                                                                                                                                                                                                                                                                                                                                                 PRA encoding smooth muscle myosin heavy chain SMI isoform - used in a vector for gene therapy for reduction of re-stenosis following coronary artery catheterisation

PRA vector for gene therapy for reduction of re-stenosis following coronary artery catheterisation

PRA sequence represents the coding sequence for the smooth muscle myosin heavy chain SMI isoform protein. This SMI coding sequence was isolated from a mouse embryo cohra library using probes based on the rabbit smooth crows myosin heavy chain SMI isoform. This sequence is included in the gene therapy vector of the invention. The vector of the invention associated adenovirus or animal-expression plasmid vector (such as pCXN2 corsists of this sequence inserted into a retrovirus, adenovirus; and male associated adenovirus or animal-expression plasmid vector (such as pCXN2 corp. PAGE208). The vector can be used in the gene therapy treatment of allowing coronary artery catheterisation for widening of sclerotic
                                                      25-MR-1997 (first entry)
Coding sequence for smooth muscle myosin heavy chain SM1.
Smooth muscle; myosin heavy chain; SM1 isoform; rabbit; arteriosclerosis; gene therapy; mouse; SM2 isoform; retrovirus; adenovirus; restenosis; associated adenovirus; coronary artery catheterisation; sclerotic artery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ICCAGCTICCTGGAATTGCTIGAAAAGCTCTGCCTCCTCCATCTCCCTTCAGGGACC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PTD04 encoding conA.

Human PTD04 encoding CNBA.

PTP04; PTP05; PTP10; SAD; ALF, ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29.4; DB 1; Length 6175;
Pred. No. 7.9;
0; Mismatches 51; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 AGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-1996, J00134.
25-JAN-1995, JP-01008s.
(OSAP) OSAR PREPECTURAL GOVERNMENT.
(VESS-) VESSEL RES LAB CO LTD.
ATARAWA E, HASGEGAWA K, ISHLYAMA H, MATSUGA Y, OGA S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1856 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1455 C;
             T34291/c
ID T34291 standard; cDNA to mRNA; 6175 BP.
                                                                                                                                                                      Location/Qualifiers
105. .6023
/*tag= a
/product= SM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
53. .2476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V81742/C

V81742/C

AC V81742.

DT 10-MAR-1999 (first entry)

DE Human PrP04 encoding CDNA,

WW PrP04; PrP04 encoding CDNA.

KW PRP04; PrP05 encoding CDNA.

KW type I receptor serine/threenine.

KW PATKINSON'S disease; Huntington'S CS Homo sapiens.

FR Key CDS 53. 2476

FT CDS 53. 2476

PN WO9849317-A2.

PP WO98049317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1846 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 12.6%;
1 Similarity 54.1%;
60; Conservative (
                                                                                                                                                                                                                                                                                                                           Arakawa E, Haseqawa K,
Sugawara M, Takahashi K;
WPI, 96-362693/36
P-PSDB; W00024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6175 BP;
                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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The prevention of cancer and neurodegenerative disease

Prevention of cancer and neurodegenerative disease

Claim 2; Page 145-146; 193pp. English

Claim 2; Page 145-146; 193pp. English

Claim 2; Page 145-146; 193pp. English

Catids encoding PrP04, SAD, PrP05, PrP10, ALP and ALK-7 proteins. The

Catids encoding PrP04, SAD, PrP05, PrP10, ALP and ALK-7 proteins. The

Craids encoding PrP04, SAD, PrP05, PrP10, ALP and ALK-7 proteins. The

Craids encoding PrP04, SAD, PrP05, PrP10, ALP and ALK-7 proteins. The

Craids encoding PrP04, SAD, PrP05, PrP10, ALP and ALK-7 proteins. The

CRALT, are protein tyrosine phosphatases (PrPs) and are used to identify

CRALT, are protein tyrosine phosphatases (PrPs) and are used to identify

CRALT, are protein tyrosine phosphatases (PrPs) and are used to identify

CRALT, are protein tyrosine phosphatases (PrPs) and are used to treat

CRALT, are protein tyrosine phosphatases (PrPs) and are used to treat

CRALT, are protein tyroson in vitro. These substances are used to treat

CRALT, are protein tyroson in vitro. These substances are used to promote neuronal survival,

CRALT, are protein tyroson and the promote neuronal survival,

CRALT, are protein tyroson as probes to identify and clone related sequences;

CRALT, are protein-encoded RNA; to generate transgenic animals and in

CRALT, are protein tyroson are used to determine the

CRALT, are protein-encoded RNA; to generate transgenic animals and in

CRALT, are protein tyroson are proper tyroson are used to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 TGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 TCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAAC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cona cione coding polypeptide - showing IgE bond factor activity. Disclosure; Page 29; 33pp; Japanese. The clone encodes a polypeptide which shows IgE binding factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 TIGAAAAGCICTGCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCTC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1083 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 3580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-APR-1991 (first entry)
Clone 23B6pl02 encoding polypeptide with IgE binding factor
activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       618 G;
                                                                                                                                                              Jallal B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB l,
Pred. No. 8.6;
0; Mismatches
20-MAY-1997; US-047222.
11-JUN-1997; US-049477.
11-JUN-1997; US-049914.
(SUGE-) SUGEN INC.
App H, Clary D, Courtneidge SA, Hui TH, Jal
Markby D, Onrust S, Peles E, Plowman GD;
WPI: 99-009434/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody; immunoglobulin; ss.
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1213 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N70646 standard; cDNA; 5018 BP N70646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
12.4%;
Best Local Similarity 48.0%;
Matches 83; Conservative (
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This is the nucleotide sequence encoding the human TATA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            holoenzyme;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3933 TTGTTTGATAATAGAGGGGGGAGAATTGTTAGTCCTCATGTGTCCAATGGCACACAT 3874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 TGACTITGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 GGCIGCCCTIGICCICCTCTTGACCTTGGCAGCTCACATGGAACAGGGCCGGGTA 70
                                                                                                                                                                                       rara-binding procein associated protein factors - and corresponding procein associated protein factors - and corresponding nucleotide sequence and deriv. antibodies, useful in screening, diagnostics and therapeutics bisclosure; Page 94-112; 180pp; English. The TMTA-binding protein associated factor brakfizs (including specific antibodies and fusion products) are used in drug screening, apecific blochemical assays for screening compounds that agonise or antagnoise salected transcription factors involved in regulating gene expression associated with human pathology.

Sequence 5962 BP; 1764 A; 1294 C; 1501 G; 1403 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screen for cpds, that bind human TATA-binding protein associated factor - by testing ability to bind to polypeptide fragments of the factor, useful as (ant)agonists of transcription factors involved disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             742215;
27-7AN-1997 (first entry)
Human TATA-binding protein associated factor hTAFI1250 gene.
Human, TATA-binding protein; TBP associated factor; TFIID; holoenc:
RNA Polymerase II; transcription; messenger RNA; nuclear fraction;
lambda-gtil; expression library; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                 12.0%; Score 28; DB 1; Length 5962; 48.2%; Pred. No. 21; tive 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 TCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCT 174
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                                                                                                                               Tanese N;
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                                                                                                                               Ruppert S,
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/product- human TAFII250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
14. .5695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-1993; US-013412.
28-JAN-1994; US-087119.
28-JAN-1994; US-188582.
(REGC) UNIV CALIFORNIA.
Comai L, Dynlacht BD, Hoey T, Ru
Tjan R, Wang E, Weinzierl ROJ;
WPI: 96-333245/33.
                                                             28-JAN-1994; U01114.
28-JAN-1994; U0-013412.
30-JUN-1993; US-087119.
(REGC ) UNIV CALIFORNIA.
COMA1 L. DYNIACT BD. HOCY T, RUPI TJAN R. WANG E. Weitzlerl ROJ; WPI; 94-264019/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5/c
T42215 standard; cDNA; 5962 BP.
14. .5692
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                   P-PSDB; R56491
                                                04-AUG-1994.
28-JAN-1994; U
28-JAN-1993; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-1996.
28-JAN-1993;
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                                   WO9417087-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3138 CATCTGACGGCAGAACTGCTGAAATTTTTGAGACGTATAAGCTGGTCCATTATCAGTCTT 3079
                                                                                                                                                                      3138 CATCTGACGGCAGAACTGCTGAAATTTTTGAGACGTATAAGCTGGTCCATTATCAGTCTT 3079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 CCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCATCTCCCTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proble Foundary DNA clones coding for poly:peptide(s) - with sequence of mammalian immunoglobulin factor and obtd. from transformed or transfected host.

Claim 8: Page 59-64; 71pp: English.

IBF and IBF CDNA are useful in studies on the immune system.

Treatment for IgF-mediated diseases may be possible. IBF may enhance breat differentiation into an immunoglobulin-secreting cell.

Sequence 5018 BP; 1424 A; 1086 C; 1165 G; 1343 T;
                                                                                                                                     116 CCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                        Sequence of the CDNA clone 2386p10.2 encoding a polypeptide exhibiting mammalian immunoglobulin binding factor activity (IBF). Immunoglobulin E-mediated disease; therapy; B-cell differentiation; immunoglobulin E-binding factor; ss. Key Location/Qualifiers 423. 2750 /*tag- a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATR-binding protein "associated factor hTAFI1250 cDNA.
TATR-binding protein associated factor; hTAFI1250; ss; screening; diagnostic; therapeutic; gene transcription regulation.
Homo sapiens. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 12.0%; Score 28; DB 1; Length 5018;
1. Similarity 53.7%; Pred. No. 20;
58; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 CAGGGACCAGCGTCACCCTCCACCATGCAAGATCTCAACACCATGTTG 223
                                                                                                                                                                                                                          176 CAGGGACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTG 223
                                                                                                         50; Indels
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                         1165
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18-SEP-1985.
15-WAR-1985.
15-WAR-1984: US-590430.
(SCHE-) SCHERING BLOTGEH CO.
(UVJO) JOHNS HOPKINS UNIV.
(SCHE) SCHERING-BIOTECH CO.
(DNAX-) DNAX RES INST MOLEC.
MATEGER CL. ISPLEARA K, MOOFE KW, Huff TF;
WPI, 85-231663/38.
                                                                        Score 28; DB 1,
Pred. No. 20;
0; Mismatches
                         ပဲ
                         1087
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ID 070729 standard; CDNA; 5962 BP.
DC 27:WAR-1995 (first entry)
DE TATA-binding protein-associated f
KW TATA-binding protein associated f
KW diagnostic; therapeutic; gene tra
KW diagnostic; therapeutic; gene tra
FH Key
Key
                                                                                                                                                                                                                                                                                                                  0/c
N50150 standard; cDNA; 5018 BP.
                         1423 A;
                                                                        ch 12.0%;
1 Similarity 53.7%;
58; Conservative (
       See also N70645, 5018 BP; 1423
                                                                                                                                                                                                                                                                                                                                                                 27-SEP-1991 (first entry)
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Best Local S:
Matches 58
           activity.
Sequence
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                                                                             Query Match
                                                                                              Local
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NS0150/
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(TBP) associated factor (TAF) designated TAFII250. The protein is a polymerate of the FTID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. wt. of 250 kD by SDS-PAGE. A fragment (1H1), derived an estimated mol. wt. of 250 kD by SDS-PAGE. A fragment (1H1), derived from a Lanbda-grill HeLa S3 cDNA expression library screened with serum isolate the TAFII250 gene from a directional cONA library (in a manda-trill derived from HeLa cell poly(A+) RNA. The screen isolated but lacked about 1.15 kD of 53 kD which contained an extended 3 untranslated region but lacked about 1.15 kD of 5 sequence. The 5 sequence was isolated when the translated region when the translated region when the screen isolated when the translated region when the translated reg
                                                                                                                                                                                                                                                                                                                    Dy You wainly praints 19422-0.

The invention relates to purified proteins involved in transcription by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition to several nuclear fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II holoenzyme. Fraction TFIID has been shown to contains a TBP and other TRFs. Purification of TFIID has been shown to sent and the components reveals 7 proteins ranging in size from 30-250 kD. Serum raised against the TFIID fraction allowed cloning of the corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3993 GICTITICCAACICCICCICTICTICITCAIGGAACAGGGIIGGAAGGIGGGGGA 3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 TGACTITGCAACTGAAGCTGAAGGACTCTTTCTGACAAATTCCTCCTATGAGTCCAGCT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human TRIA-binding protein associated factor Nucleic acids encoding human TRIA-binding protein associated factor for production of recombinant peptide(s), used for modulating transcription of TRIS encodes human 53-78, 86pp; English. TSY596 encodes human TRIA-binding protein associated factor (TAF) polypeptide, hTAPII250 (mol. weight 250kb). TRI peptides derived from NTAFII30 alpha, NTAFII30 beta, hTAFII40, hTAFII30, hTAFII30, hTAFII30, hTAFII30, hTAFII30, hTAFII30 and hTAFII10 and nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTGCCCCTTGTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTA 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1997 (first entry) TATA-binding protein associated factor, hTAFI1250 cDNA. TATA-binding protein associated factor; TAF; nuclear protein; RNA polymerase transcription; TATA-binding protein; TBF; entranscription; TATA-binding protein; TBF; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 TCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1501 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from lambda-gtll expression libraries.
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14. .5695
/*tag= a
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28-JAN-1993; US-013412.
28-JAN-1993; US-013412.
28-JAN-1994; US-18852.
09-MAY-1996; US-646713.
(REGC ) UNIV CALIFORNIA.
Comai L. Dynlact BD, Hoey T, Rup T ian R, Wang E, Welnzierl ROJ;
WPI: 97-319113/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T79596 standard; cDNA; 5962 BP T79596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 48.29 tes 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W25020.
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them, are used to modulate transcription, including transcription initiation. TARS are nuclear proteins involved in RNA polymerase I, II and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typically a protein like TBP or another TAF, an activator, or DNA. 1403 T; Sequence 5962 BP; I764 A; TAF, an activator, or DNA.
                                                                                                                                                                                                                     3933 TITGIITGAIAAIAGAGGGGCAGAAITIGIITAGICCICAIGIGICAAIGGCACCACAI 3874
                                                                                                                                                                                                                                                              71 TGACTITGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2101 GAAAACCICCGAGAGAGAAGGCAGAAGGAGCAGTGTTCTCGTTCTTGCCCTAAGGTGGAG 2042
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-1999 (first entry) cDNA encoding a murine uncoupling protein designated mUCP3a. Mouse; mitchhondrial uncoupling protein; mUCP3; metabolic regulation; isoform; ds.
                                                                                                                                                                                                 11 GGCIGCCCTIGICCICCTCTIGACCCICCTIGGCAGCTCACAIGGAACAGGGCCGGGIA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 GAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding murine mitochondrial uncoupling polypeptide(s) - useful for producing recombinant polypeptide(s) Claim 11; Fig 2a-d; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a murine mitochondrial uncoupling protein designated mUCP3a. The protein is involved in metabolic requiation. The specification describes different isoforms of this protein.
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                                                                                                                                            DB 1; Length 5962;
21;
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                                                                                                                                                                                                                                                                                                                                              131 TCCTGGAATTGCTTGAAAGCTCTGCCTCCTCCTCCATCTCCCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                740 G;
                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.9%; Score 27.8; DI
53.2%; Pred. No. 19;
tive 0; Mismatches
                                                                                                                                         12.0%; Score 28;
1larity 48.2%; Pred. No. 2
Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              713 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240. .1166
/*tag= a
/product= mUCP3a
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
V71227/c
TD V71227 standard; CDNA; 2782 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amaral MC, Chen J, Zhang N;
WPI; 99-059063/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T95763/c
ID T95763 standard; cDNA; 2635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-1997; 937466.
25-SEP-1997; US-937466.
(TULA-) TULARIK INC.
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                                                                                                                                                     Similarity
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Best Local Similarity
Matches 59; Conserv
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P-PSDB; W85116
                                                                                                                                  Query Match
Best Local Simil
Matches 79; (
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Total division and therefore alter root development, or alter plant stem or hypocotyl gravitropism

Teal division and therefore alter root development, or alter plant stem or hypocotyl gravitropism

Claim 6: Page 130-131: 221pp: English.

Claim 6: Page 130-131: 221pp: English.

CCARECROW (SCR) SRPal2 gene, identified by homology to the rabidopsis SCR gene (see T95753). It encodes a 808-amino acid polypeptide (see W38188). SCR is expressed specifically in embryo cop progenitor tissue and in certain root and stem tissues. It root progenitor tissue and in certain root and stem tissues. It regulates a specific asymmetric division, and controls gravitropic response in earlial structures and root formation. Nucleic acid molecules (see T95753-66) encoding SCR protein sequences (see CRS753-66) encoding SCR proteins acquences (see CRS753-66) encoding SCR proteins is confered to overexpress SCR, so that call division is conceased in roots. resulting in thicker root development, while a cusceptible to lodging. Plants that contain an antisense control of a SCR promoter and expressed in a plant to prace dunder control of a SCR promoter and expressed in a plant to confer herbicide, salt, pathogen or insect resistance, or when concern herbicide, salt, pathogen or insect resistance, or when solds a salt, pathogen or insect resistance, or when solds a salt, pathogen or insect resistance, or when solds a salt, pathogen or insect resistance, or when solds and salt and salts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2301 GATÍCTGCATCATCCTTCTCAAGCGGAAGCTGTCTAAATCCGGCTCGGATCAGTCTCG 2242
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Dentatorubral-pallidoluysian atrophy cDNA (nucleotides 238-2090).
Glyceraldehyde-3-phosphate dehydrogenase; GAPDH; polyglutamine;
CAG repeat domain; neurodegenerative disorder; inhibition; DRPLA;
Huntington's disease; schizophrenia; psychiatric disorder;
dentatorubral-pallidoluysian atrophy; ss.
              Arabidopsis SCARECROW clone SRPal2.
SCARECROW, SCR: SRPal2 gene; transgenic plant; root; gravitropism; crop improvement; ss.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 2635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           778 T;
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50.8%; Pred. No. 21;
tive 0; Mismatches 64; Indels
                                                                                                                                                                                                COUNTY) UNIV NEW YORK STATE.
Benfey PN, Dilaurenzio L, Helariutta Y, Malamy JE, Pysh L, Wysocka-Diller J;
Pysh L, Wysocka-Diller J;
Pysh L, 97-5496883550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            623 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 C;
                                                                                  Location/Qualifiers 3. .2429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 50.89
Matches 66; Conservative
                                                                                                                                                                           US-842445.
US-638617.
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                                                                                                                                                             25-APR-1997; U07022
                                                                                                                                   WO9741152-A1.
06-NOV-1997.
                                                                                                                                                                             24-APR-1997;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Human gene P2XM whose transcription is induced by p53 - useful, e.g.

Human gene P2XM whose transcription is induced by p53 - useful, e.g.

for diagnostic purposes and in development of new anticancer drugs

Claim 2: Rage 22-23; 43pp; Japanese.

Claim 2: Rage 22-23; 43pp; Japanese.

Claim 2: Rage 22-23; 43pp; Japanese.

This sequence represents the coding sequence for the P2XM protein of the receptors, and (ii) RP-2 protein which is expressed in thymocytes of APP receptors, and (ii) RP-2 protein which is expressed in thymocytes of APP receptors, and (ii) RP-2 protein which is expressed in thymocytes of APP receptors, and (ii) RP-2 protein which is expressed in thymocytes of APP receptors, and (ii) RP-2 protein which is specifically required by the tumour-suppressor gene p53. The P2XM gene is specifically required by the tumour-suppressor gene p53. The P2XM gene is specifically expressed in skeletal muscle and sequence losses frequently occur in rhabdoid sarcomas. The genes may be used for diagnostic purposes (e.g. by detecting changes occurring in the gene in sarcomas), using probes and primers containing to the development of new anticoncer drugs.

C in the development of new anticoncer drugs.

Sequence 1293 BP; 271 A; 379 C; 389 G; 254 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAPDH
                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Columms 21-24; 19pp; English.

Example 7; Columms 21-24; 19pp; English.

This sequence represents dentatorubral-pallidoluysian atrophy (DRPLA) cDNA (nucleotides 238-2090 of Genbank accession number D38529). The invention relates to a new screening assay for compounds capable of inhibiting binding of glyceraldehyde-3-Phosphate dehydrogenase (GAPDH) to polyglutamine. The assay comprises providing an aqueous solution containing a test compound, polyglutamine-containing molecules and GAPDI molecules is reduced in the presence of the test compound. Inhibitors identified by the above assay could be used to treat neurodegenerative diseases or psychiatric disorders caused by a gene containing an extended CAG domain, e.g. Huntington's disease or schizophrenia. sequence 1853 BP; 347 A; 774 C; 388 G; 344 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 TCCTCCTATGAGTCCAGCTTCCTGGAATGCTTGAAAAGCTCTGCCTCCTCCATCTC 171
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                                                                                                                                                                                                                                                                 Serieming assay for inhibitors of GAPDH binding to poly;glutamine for use in treating neuro-degenerative diseases or psychiatric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-ARR-1999 (first entry)
Coding sequence for human p53 regulated protein, P2XM.
Umman; p53 regulated protein; P2XM; ATP receptor; RP-2 protein;
thymocyte; apoptosis; tumour-suppressor gene; rhabdoid sarcoma;
anticancer drug; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.8%; Score 27.6; DB 1; Length 1853; Best Local Similarity 56.7%; Pred. No. 18; Matches 51; Conservative 0; Mismatches 39; Indels 0;
                                                                                                                                                            Burke JR, Enghild J, Strittmatter WJ, Vance JM, WPI; 98-178475/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000 CCTCCCCCAACAAGCCTCTCTGTCTCCAAT 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 CCTTCAGGGACCAGCGTCACCTCCACCAT 201
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26-WAR-1997; JP-093044.
(SARA) OTSURA PHARM CO LTD.
Nakamura Y, TOKINO T;
WPI; 98-532006/45.
P-PSDB; W76434.
03-MAR-1998.
03-NOV-1995; 553110.
03-NOV-1995; US-553110.
(UYDU-) UNIV DUKE.
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WO9842835-Al.
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Ouery Match 11.8%; Score 27.6; DB 1; Length 1293; Best Local Similarity 58.5%; Pred. No. 16; Matches 48; Conservative 0; Mismatches 34; Indels 0;
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196 CACCATGCAAGATCTCAACACC 217 11 | 1 | 1 | 1 | 1 | 1 507 CACGGGCACCAACTCCAGATC 486

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Search completed: March 20, 2000, 09:31:54 Job time: 1077 sec

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Appli
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                                                                                         March 18, 2000, 15:56:36 ; Search time 61.26 Seconds (without alignments) 457.314 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Sequence 1, Sequence 2, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 5, Sequence 5, Sequence 6, A Sequence 1, A Sequence 2, A Sequence 9, A Sequen
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234
1 ATGGGGTCTGGGGCTGCCCT.....ACCATGITGTCTGCAACACA 234
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. /cgn2_6/ptodata/2/ina/3A_COMB.seq:*

. /cgn2_6/ptodata/2/ina/5D_COMB.seq:*

. /cgn2_6/ptodata/2/ina/5D_COMB.seq:*

. /cgn2_6/ptodata/2/ina/5D_COMB.seq:*

. /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*

. /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*

. /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*

. /cgn2_6/ptodata/2/ina/PCTUS9_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214294 seqs, 59861208 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                           Issued_Patents_NA:*
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37895
8268
37895
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                                                                                                                                                           Title:
Perfect score:
Seguence:
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272222738
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                                                                                            Run on:
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Sequence 2, Ap Sequence 2, Ap Sequence 79, A Sequence 79, A Sequence 2, Ap Sequence 1, Ap Sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: VA
SURME: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: FICHOPPY disk
COMPUTER: PAC COMPATIBLE
COMPUTER: PAC COMPATIBLE
COMPUTER: PAC COMPATIBLE
COMPUTER: PAC COMPATIBLE
SOFTWARN: PAC COMPATIBLE
APPLICATION NUMBER: US/08/232,463
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
APPLICATION NUMBER: 29,768
RATORNEY/AGENT INFORMATION:
NAME: BERY, SEEPENDEN A.
RECISTRATION NUMBER: 29,768
REFERENCE/COCKET NUMBER: 30472/114 IMMU
TELLEPKA: (703)836-9300
TELLEPKA: (703)863-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: FARKNER, F. G.
TILLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Disgonal Road, Suite 500
CITY: Alexandria
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERA: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
TOPOLOGY: 11near
IMMEDIALE SOURCE:
22496
22496
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US-08-232-463-14
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Matches 8; Conserva
RESULT 1
US-08-232-463-14
Query Match
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Gaps

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90; Indels

1 ATGGGGTCTGGGCTGCCCTTGTCCTCTTGACCCTCTTGGCAGCTCACATGGAACA 60

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US-08-254-359A-2 US-08-477-407-9

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Query Match
Best Local Similarity
Matches 79; Conserva
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MOLECULE TYPE:
                         S-08-188-582-10/c
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; LOCATION:
US-08-188-582-10
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                                                                                                             61 GGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTAT 120
                                                                                                                                                                                                                                                                     121 GAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGG 180
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Sequence 8, Application US/08750357

Sequence 8, Application US/08750357

Sequence 8, Application US/08750357

Sequence 8, Application US/08750357

SEQUENCE 1 INFORMION:

APPLICANT: WILLIAMS, MATK

APPLICANT: USE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN

TITLE OF INVENTION: MALE STERILE PLANTS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

STREE: YOU BEN 1404

STREE: VIFGILLA ADDRESS:

STREE: VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.2%; Score 28.6; DB 5; Length 2
Best Local Similarity 61.3%; Pred. No. 3;
Matches 46; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTGTCT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTIN ND DATA:
APPLICATION NUMBER: US/08/750,357
FILLIG DATE: 21-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MCGOWAN, MALCOIM K.
REGISTRATION NUMBER: 90,300
REFERRUCE/DOCKET NUMBER: 018030-100
RELECOMMUNICATION HIPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: DNA (genomic) US-08-750-357-8
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TELERAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2662 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States ZIP: 22313-1404
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STRANDEDNESS: sinc
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APPLICANT: Hoey. Timothy
APPLICANT: Tanese, Timothy
APPLICANT: Tanese, Naoko
APPLICANT: Tanese, Naoko
APPLICANT: Tanese, Naoko
APPLICANT: Tanese, Naoko
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVERTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVERTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVERTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVERTION: WIGLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: A Embarcadero Center, Suite 3400
STATE: California
COUNTRY: USA
ZIP: 9411-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3993 GTCTTTCCAACTCCTCCTCCTGTTCTTCTGTCAIGGCAACAGGGTTGGAAGGTGGCGCA 3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 IGACTITGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.0%; Score 28; DB 1; Length 5962 ilarity 48.2%; Pred. No. 6.9; Conservative 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 TCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCTCCCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER EACACHLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
FILING DATE: 28-JAN-1994
CLASSIFICATION NUMBER: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 398-1989
TELERAX: (415) 398-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-646-715-10/c
; Sequence 10, Application US/08646715
Sequence 10, Application US/08188582
Patent No. 5534410
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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FILING DATE:
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GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Comai, Lucio
APPLICANT: Heey Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Rang, Edith
APPLICANT: Wang, Edith
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3933 TTTGTTTGATAATAGAGGGGGGAGAATTTGTTAGTCCTCATGTGTCCAATGGCACCACAT 3874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 TGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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Best Local Similarity 48.2%; Pred. No. 6.9;
Matches 79; Conservative 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USALILOCULAGE

COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PELENTIN DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 28-JAN-1994
APTORNEY/AGENT INFORMATION:
NAME: OSMUN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
FELEROM/UNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEROME (415) 398-3249
INFORMATION FOR EQ. ID NO: 10:
SEQUENCE CHARRACTERISTICS:
LENGTH: 5962 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOTOCY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 | 11 | 1 | 1 | 3833 GCCCACATITCAGITITAGGICAGGACGCICCTICAITITICIT 3830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 TCCTGGAATTGCTTGAAAGCTCTGCCTCCTCCTCCATCTCCCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-937-466-1/c
; Sequence 1, Application US/08937466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14..5692
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MOLECULE TYPE: CDNA
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; LOCATION: 14..
US-08-646-715-10
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APPLICANT: Tables, Ming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.8%; Score 27.6; DB 2; Length 1853;
Best Local Similarity 56.7%; Pred. No. 5.5;
Matches 51; Conservative 0; Mismatches 39; Indels 0.
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Patent No. 5670319

GENERAL INFORATION:

APPLICANT: Goeddel, David V.

APPLICANT: Rothe, Mike

TITLE OF INVENTION: Tumor Necrosis Factor

TITLE OF INVENTION: Receptor-Associated Factors

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA
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ZIF: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: STEM: PC-DoS/MS-DOS
SOFTWARE: Patin (genentech)
CURRENT APPLICATION NATE:
APPLICATION NUMBER: US/08/331,394
FILING DATE: 27-MAY-1994
ATTORNEY AGENT INFORMATION:
NAME: DFGGGT: 27-MAY-1994
ATTORNEY AGENT INFORMATION:
RECISTRATION NUMBER: 33,055
RECISTRATION NUMBER: 31,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 1000 CCTCCCCAACACCTCTCTGTCTCCAAT 1029
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INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1883 base pairs TYPE: nucleic acid STRANDEDNESS: aingle TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: single
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US-08-331-394-3/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 GAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCT 115
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Sequence 2, Application US/08553110

Batent No. 5723301

GENERAL INFORMATION:

APPLICANT: Burke, James R.

APPLICANT: Enghild, Jan

APPLICANT: Enghild, Jan

APPLICANT: Enghild, Jan

APPLICANT: Enghild, Jan

APPLICANT: Stiffmatter, Warren J.

APPLICANT: Stiffmatter, Warren J.

APPLICANT: Stiffmatter, Warren J.

APPLICANT: Stiffmatter, Warren J.

CORRESPONDENCE ADDRESS:

ADDRESSED: ADDRESS:

ADDRESSED: Kenneth D. Sibley

STRET: P.O. Drawer 34009

CITY: Charlotte

STRET: P.O. Drawer 34009

CITY: Charlotte

STRET: P.O. Drawer 34009

COUNTRY: United States of America

2IP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPPOTER: BR PC compatible

COMPUTER: BR PC compatible

COMPUTER: PRICATION DATA:

STERM: APPLICATION DATA:

FILING DATE:

STATEST DATE:

FILING DATE:

FILING DATE:

STATEST DATE:

FILING DATE:

FILING DATE:

STATEST DATE:

FILING DATE:

FILING DATE:

FILING DATE:

STATEST DATE:

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STATEST DATE:

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53.2%; Pred. No. 5.7;
tive 0; Mismatches 52; Indels 0
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                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
ATTORITYAGENT INFORMATION:
NAME: 51bley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/TOCKET WUMBER: 5405-117
TELECOMMUNICATION:
TELECHONE: 919-420-2200
                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T97-009
                                                                                                                                                                                                                          FILING DATE:
CLASSITICATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSNAN, RICHARD 8, 627
REFERENCE/DOCKET NUMBER: 36, 627
RELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-434
ITELEPRAK: (650) 343-434
ITELEPRAK: (650) 343-434
ITELEPRAK: (650) 343-434
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ITELEPRAK: (7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.2'
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear ; MOLECULE TYPE: CDNA US-09-172-528-1
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RESULT 7 US-08-553-110-2

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APPLICANT: Goeddel, David V.

PAPLICANT: Rothe. Mike
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
STREET: 460 Point San Bruno Blvd
GITY: South San Francisco
CITY: South San Francisco
CUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08744139
Patent No. 5869612
GENERAL INFORMATION:
APPLICANT: GOEddel, David V
APPLICANT: Rothe, Mike
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECPTOR-ASSOCIATED FACTORS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Genented, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 GAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     905 GACAAIGITCTCAAAGGTTGCTATCTTCTGCTCCAAAATCTGGCACCGCTGGAGTAGCTC 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 2121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 5 25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
APPLICATION NUMBER: US/08/446,915
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/250858
FILING DATE: 27-MAY-1994
PRIOR APPLICATION NUMBER: 08/331394
FILING DATE: 28-DAY-1994
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: 08/331394
ATTORNEY AGENT INFORMATION:
ANNEY AGENT A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.6%; Score 27.2; Di
Best Local Similarity 53.8%; Pred. No. 8;
Matches 56; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
REFERENCE,DOCKET NUMBER: 897E;
TELECOMMUNICATION INFORMATION:
TELEPRONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2121 bases
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
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US-08-446-915-3
                                                                                                                                                                                                                                                                                                                                                   94080
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APPLICANT: Goeddel, David V.
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
LIP: 94080
                                                                    94 GAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 11.6%; Score 27.2; DB 2; Length 2121; Best Local Similarity 53.8%; Pred. No. 8; Matches 56; Conservative 0; Mismatches 48; Indels 0
                                                                                                                                                    154 TGCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCTCCA 197
                                                                                                                                                                                                             845 IGGCCCCACCIGGITCAAGGITCCIGGAAGGCITGGGCCTCCA 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 TGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION MATA:
APPLICATION MATA:
APPLICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08250858 Patent No. 5708142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA.
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreder: Ginger R.
RESISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897.1
TELEPHONE: 415/255-3216
TELEPHONE: 415/255-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-08-446-915-3/c
: Sequence 3. Application US/08446915
; Patent No. 5741667
; GENERAL INFORMATION:
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TELEX: 910,371-7168
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2121 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 11near
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94 GAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTC 153
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11.6%; Score 27.2; DB 6; Length 2121;
Best Local Similarity 53.8%; Pred. No. 8;
Matches 56; Conservative 0; Mismatches 48; Indels 0.
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US-08-101-53-5
US-08-101-53-5
US-08-101-53-5
US-08-101-53-5
US-08-101-53-5
US-08-101-53-5
US-08-101-53-5
US-08-101-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       845 TGGCCCCACCTGGTTCAAGGTTCCTGGAGAGGCTTGGGCCTCCA 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 TGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCA 197
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IIP: 90012-5628

COMPUTER READALE FORM:
MEDIOUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OFFILCATION NOTHER: US/08/101,593
FILING DATE: 19930802
CIASSIFICATION NOTHER: US/08/101,593
FILING SATTONINGER: US/08/101,593
FILING SATTONINGER: 19930802
CIASSIFICATION NOTHERS: 199308
REGISTRATION NOTHERS: 190305
REGISTRATION NOTHERS: 1920-305
REGISTRATION NOTHERS: 1920-305
FELECOMMUNICATION HECRMATION:
REFERENCE/DOCKET NUMBER: 8971
TELEPHONE: 415/225-3216
TELEPHONE: 415/225-3216
TELERA: 415/952-9881
TELER: 910/771-7168
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2121 bases
TYPE: nucleic acid STANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEBRANE: (213) 977-1001
TELEBRAN: (213) 977-1003
INFORMATION FOR SED ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 2459 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 108 .2456
                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
PCT-US95-06639-3
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US-08-101-593-5
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GENERAL INFORMATION:
APPLICANT: GENERAL INFORMATION:
TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
NUMBER OF SEQUENCES: 66
CORRESPONDENCES: 66
CORRESPONDENCES: 66
CORRESPONDENCES: 66
CORRESPONDENCES: 66
CORPUTER: Generatech. Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COMPUTER: 105A
21P: 94080
COMPUTER: 3.5 Inch, 1.44 Mb disk
MEDIUM TYPE: 3.5 Inch, 1.44 Mb disk
COMPUTER: 3.5 Inch, 1.44 Mb disk
COMPUTER: BALIN Generateh)
COMPUTER: BALIN Generateh)
COMPUTER: PALIN Generateh)
COMPUTER: PALIN Generateh)
COMPUTER: PALIN Generateh)
COMPUTER: DALIN GENERAL POST/US95/06639
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11.6%; Score 27.2; DB 3; Length 2121;
Best Local Similarity 53.8%; Pred. No. 8;
Matches 56; Conservative 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 TGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCA 197
        MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IMP PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genenceh)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,139
FILING DATE: 31-Oct-1996
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250858
FILING DATE: 05/27/1994
ATORNEY AGENT INFORMATION:
NAME: DIEGET, GINGER: 33,055
REGISTRATION NUMBER: 33,055
REGISTRATION NUMBER: 33,055
REGISTRATION NUMBER: 33,055
TELEPHONE: 415/25-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/250858
FILING DATE: 77-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/31394
FILING DATE: 28-CGT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415/952-9881
TELEX: 910/31-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: Linear
US-08-744-139-3
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CLASSIFICATION:
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PCT-US95-06639-3/c
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                                                                                                            1598 TGCCTTTTATGGCGTGGTCGGCACCACCGCCTGCCGCTTTCGATCCGCGGCTGGCATC 1657
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                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/0846595A

Patent No. 566080

GENERAL INFORMATION:
APPLICANT: MYTON F. Goodman
APPLICANT: MYTON F. Goodman
APPLICANT: Linda J. Reha Krantz
TILLE OF INVENTION: METHODS FOR IDENTIFYING AND ISOLATING:
TILLE OF INVENTION: WRIANT T4 POLYMERASES
NUMBER OF EXCURNION: METHODS FOR IDENTIFYING AND ISOLATION: ARIANT T4 POLYMERASES
CORRESPONDENCE ADDRESS:
ADDRESSEE: RObbins, Berliner & Carson, LLP
STREET: 201 No. 5660980th Figueroa Street, Suite 500
CITY: Los Angeles
STREET: 201 No. 5660980th Figueroa Street, Suite 500
CITY: Los Angeles
STREET: 201 No. 5660980th Figueroa Street, Suite 500
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS FISHER: US/08/465,995A
FILICATION NUMBER: US/08/465,995A
FILICATION NUMBER: US/08/465,995A
FILICATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 1920-305D2
TELECOMMUTCATION NUMBER: 1920-305D2
TELECOMMUTCATION NUMBER: 19377-1001
TELEFAX: 213/977-1003
TELEFAX: 213/977-1003
TELEFAX: 213/977-1003
TELEFAX: 213/977-1003
TELEFAX: Z13/977-1003
TELEFAX: Z13/977-1003
TELEFAX: Z13/977-1003
TELEFAX: Z13/977-1003
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11.5%; Score 27; DB 1; Length 2459;
Best Local Similarity 56.0%; Pred. No. 9.9;
Matches 51; Conservative 0; Mismatches 40; Indels
                                   40; Indels
Best Local Similarity 56.0%; Pred. No. 9.9;
Matches 51; Conservative 0; Mismatches
                                                                                                                                                                                                      1658 GICGATCACCATGCGTGGTCATCAGATCATG 1688
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                                                                                                                                                                        190 ACCCTCCACCATGCAAGATCTCAACACCATG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: line...
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108..2456
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US-08-465-995A-5
                                                                                                                                                                                                                                                                                                                        US-08-465-995A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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PREPLICANT: LINEA F. COODMAN

PREPLICANT: LINEA F. COODMAN

APPLICANT: LINEA F. COODMAN

APPLICANT: LINEA F. COODMAN

APPLICANT: LINEA ADDRESS:

OUNDESS OF SEQUENCES:

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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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93.2
75.8
36.4
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                                                                                                                        March 19, 2000, 08:46:58; Search time 538.4 Seconds
(without alignments)
1640.983 Million cell updates/sec
                                                                                                                                                                                                                   US-09-092-296-7_COPY_51_284
234
1 ATGGGGTCTGGGCTGCCCT.....ACCATGITGTCTGCAACACA 234
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                             4538634 seqs, 1887831982 residues
                                                                                   OM nucleic - nucleic search, using sw model
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em_est2:*
em_est2:*
em_est3:*
em_est3:*
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em_est7:*
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em_est13:*
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em_est16:*

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gb_est27:*
gb_est28:*
gb_est28:*
gb_est39:*
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gb_est13:*
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gb_est15:*
gb_est16:*
gb_est17:*
gb_est18:*
gb_est18:*
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gb_est21:*
gb_est22:*
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gb_est24:*
gb_est25:*
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9b_est31:*
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A1857998 wj69b01.x A0136529 UT.R-C2P-A0718761 HS_5511_B AA282040 ZSB903.5 A5334569 ff77c11.s AA741185 cb30a02.s AA741185 cb30a02.s

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Description

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/dev_states"adult"
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Fax: 319 315 9565
Bmail: msoarcs@blue.weeg.ulowa.edu
The sequence tag present in the CDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult Lung ilbrary. CDNA Library Preparation: M. Fathma Bonaldo, Ph.D. Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Norway rat.
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eukheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases I to 328)
Bonaldo,M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                           1. 404
Abcardism="Homo sapiens"
Abcard="taxon:9606"
Aclone="taxon:9608"
Aclone="taxon:9608"
Aclone="taxon:9608"
Aclone="taxon:0008"
Aclone="taxon"
Alssue="taxon"
Adifferentiated (4 pooled tumors, including primary and metastentis"
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UI-R-C2P-nq-e-02-0-UI.s1 UI-R-C2P Rattus norvegicus CDNA clone
UI-R-C2P-nq-e-02-0-UI 3', mRNA sequence.
AI136523 GI:3637300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 74.8%; Score 175; DB 61; Length 404; Best Local Similarity 99.4%; Pred. No. 6.6e-41; Matches 175; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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      Seg primer: -400P from Gibco
High quality sequence stop: 395.
Location/Qualifiers
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eukaryota: Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Euthoria: Lorder interpression of the concert of th
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A1081365 Pat.pk005
A0373905 RPCIII-14
M890413 ELL14A7 Chr
R90433 16788 Lambd
T74483 8146 Lambd
T74643 11421 Lambd
T76564 11421 Lambd
T76564 11421 Lambd
T44613 7876 Lambd
A102852 W183802.x
A1042852 W183802.x
T52782 yap761.r1
T52782 yap761.r1
T41525 1106 Lambd
A1803834 tp30412.x
A142028 sa66f12.y
A142028 sa66f12.x
A143019 yaf5601.r1
T59783 yb66c04.r1
R3443415 yaf57966.r1
AA444415 yaf57908.r
A1243415 x87008.r
A1243415 x87008.r
A1243415 x87008.r
A1243415 x87008.r
A1243415 x87008.r
A1018775 ov32e12.x
A1829206 wK76f01.x
A1010074 EST204525
T41524 10105 Lambd
AA991822 ot45c07.s
AM01353 116028 W
A0718755 NS. 5511_B
A1757641 ea33d07.y
A7740265 NS. 5511_B
A1757641 ea31d07.y
T41533 10116 Lambd
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AQ290553
AQ373909
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AI219495
AI692905
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AI010074
T41524
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T59783
R34436
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A1857998
A1857998.1 GI:5511614
         human.
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RESULT 1 AI857998/c LOCUS DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS

JOURNAL

REFERENCE

5

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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-388
Tel: (206) 6
       (eller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA282040 331 bp mRNA EST 14-AUG-1997 zs99a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704620 3',
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Eucharia; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tunor Gene Index 1919.

On Dep 12, 1996 this sequence version replaced gi:1402231.

On Sep 12, 1996 this sequence version replaced gi:1402231.

Contact: Robert Strausberg, Ph.D.

Email: 80bert_Strausbergehih, gov
This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -41m13 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
153 c 124 g 117 t 17 others
                                                                           Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                 scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .552
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/clone="Plate=1087 Col=18 Row=L"
/clone_llb="RPCI-11 Human Wale BAC Library"
/sex="male"
                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 CTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCT 152
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AA282040.1 GI:1924872
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Best Local Similarity 86.59
Matches 83; Conservative
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/clone="UI-R-Cap"
/clone="UI-R-Cap"
/clone="UI-R-Cap"
/clone="UI-R-Cap"
/do_stage="ddut"
/lab_host="Dilib" (Life Technologies)"
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Makaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 552)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS_551_B2_F09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate-1087 Col-18 Row-L, genomic survey sequence. AQ718761.1 GI:5468077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 GCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGGTGAAGGAGTCTTTTC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 TGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCC 163
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Live 0; Mismatches 58; Indels

    .328
    /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
    /db_xref="taxon:10116"

                      Seq primer: M13 Forward.
Location/Qualifiers
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Best Local Similarity 68.89
Matches 128; Conservative
Genetics
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/clone="IMAGE:55940"
/clone="IMAGE:55940"
/clone="IMAGE:55940"
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/tissue_type="colon"
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/note="vector: pT73D-Pac (Pharmacia) with a modified
polylanker; Site_i: Not I; Site_2: Eco RI; lst strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA
vas prepared to Eco RI adaptors (Pharmacia), digested with Not
I snd cloned into the Not I snd Eco RI sites of the
modified pT773 vector. Library went through one round of
normalization:
39 a 108 c 94 g 153 t
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Eutheria: Primates; Cstarrhini; Hominidae; Homo.
I (bases 1 to 424)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Csncer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone="IMAGE:1352162"
/clone="IMAGE:1352162"
/lasue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
On Jan 5, 1998 this sequence version replaced gi:2581148.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                         ch 15.6%; Score 36.4; DB 34; Length 494; 1 Similarity 56.8%; Pred. No. 1.3; 67; Conservative 0; Mismatches 51; Indels 0;
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Location/Qualifiers
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Insert Length: 742 Std Error: 0.00
                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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AA741185
AA741185.1 GI:2779777
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrats; Mammalla;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

E 1 (bases lto 494)
S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NRICOAD http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
L Oppublished (1997)
On May 9, 1995 this sequence version replaced gi:802984.
Contsct: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue_Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M.D., Ph.D. cDNA Library Preparation: M. Bento Sogres, Ph.D. cDNA Library Arraying: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Gencme Sequencing Dy: Washington University Gencme Sequencing Center DNA Sequencing NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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AA534569 AA534569.1 GI:2278822
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Pred. No. 1.2;
0; Mismatches 51; Indels 0;
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High quality sequence stop: 370.
Location/Qualifiers
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                                                        /organism="Homo sapiens"
/db_xref="GDB:5854344"
High quality sequence stop: 242.
Location/Qualifiers
                                                                                                  /db_xref="taxon:9606"
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56.8%;
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AA534569/c
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On Jan 17, 1998 this sequence version replaced gi:2045507.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausbergenih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Finant: Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CNA Library Arrayed by: Greg Lennon, Ph.D.

CNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NcI-GAP clone distribution information can be www-bio.linl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA936790 402 bp mRNA EST 19-MAY-1998 oh89a02.sl NCI_CGAP_C08 Homo sapiens CDNA clone IMAGE:1474154 3'
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1 (bases 1 to 40; Catarrhini; Hominidae; Homo.

NCI-GAP http://www.ncbi.nlm.nlh.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                    87 GCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGA 146
                                                                                                                                                                                                                                                             303 GATGATGTACTGTCATATATAAATCCACTAAATCCAGTACCAGGAACTGCCTGG 244
                                                                                                                                                                                         Gaps
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                                                                                                                                   Score 36.4; DB 38; Length 424;
Pred. No. 1.3;
0; Mismatches 51; Indels 0;
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Seq primer: -40m13 Wed, ET from Amersham
High quality sequence stop: 386.
Location/Ovalifiers
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/db_xref="taxon:9606"
/clone="IxA62:1474154"
/clone=lib="NCI_CGAP_CO8"
/tlssue_type="adenocarcinoma"
/lab_host="DH10B"
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1 Similarity 56.8%;
67; Conservative C
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Best Local Si
Matches 67;
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AA936790/c
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Score 36.4; DB 40; Length 402;

15.6%;

Query Match

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Tunor Gene Index

Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797652.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington Onliversity Genome Sequencing Center
Clone distribution: NGI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 1493 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality Sequence stop: 451.

Location/Qualifiers

1. 529
Cyrganism="Momo sapiens"

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/clone="IMAGE:1639054"
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//lab_host="bH10B"
//lab_host="DH10B"
//lab_host="primer: Sire_1: Not I; Sire_2: Eco RI; lst strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
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ov32e12.x1 Scares_test1s_NHT Homo sapiens cDNA clone IMAGE:1639054
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1 (bases 1 to 523 10 to 523 NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                             87 GCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGA 146
                                                                                                     296 GATGATGTACTGTCATATATAAATCCACTAAATCCAGCTACCAGGAACTGCCTGG 237
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  56.8%; Pred. No. 1.2;
ive 0; Mismatches 51; Indels
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Best Local Similarity 56.8 Matches 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                           RESULT 8
AI018775/c
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TITLE
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RESULT 9 A1829206/c LOCUS KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

ACCESSION VERSION

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1 (Dases 1 to 545)
Newman, T., debuljn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T41524 545 bp mRNA EST 07-AUG-1995
10105 Lambda-PRLZ Arabidopsis thallana cDNA clone 100A7T7, mRNA
sequence.
T41524
T41524.1 GI:931185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 TCCATCTCCCTTCAGGGACCAGCGTCACCTCCACCATGCAAGATCTCAACACCATGTTG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Jan 24, 1995 this sequence version replaced gl:634112.
Contact: Thomas Newman Assured the Santa Research Laboratory
MSG-Dob Plant Research Laboratory
Michigan State University
MSG-Dob-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp.
Rattus sp.
Rattus sp.
Rattus sp.
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 190)
1 Lee.N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Rerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (RESI) Catalog & F
                                                                                                                                                                                                                                                                         Unpublished (1998)
On Jan 19, 1998 this sequence version replaced gi:2150555.
Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 69.7%; Pred. No. 4.7;
Matches 46; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 190
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RLUBT18"
/clone_lib="Normalized r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lansing,M1
Tel: 517-353-0854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thale cress.
                                                                                                                                                                                                                                              Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 CCTGCA 125
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T41524
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DEFINITION
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COMMENT
      SOURCE
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Human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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EST204525 Normalized rat lung, Bento Soares Rattus sp. cDNA clone
RLOBT38 3' end, mRNA sequence.
AIO10074
AIO10074.1 GI:3223906
EST.
                                                                                                                                                                                                                                                                                   AI829206 451 bp mRNA EST 26-AUG-1999
wk76f01.xl NCI_CGAP_Panl Homo sapiens cDNA clone IMAGE:2421337 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 GAIGAIGIACIGIACIGICAIAIAIAAAICCACIAAAICCAGCIACCAGGAACIGCCIGG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 GCTGAAGGAGTCTTTTCTGACAATTCCTCCIATGAGTCCAGCTTCCTGGAATTGCTTGA 146
      299 GATGATGTACTGTACTGTCATATATAAATCCACTAAAATCCAGCTACCAGGAACTGCCTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 AAAGCICICCICCICCAICICCCIICAGGACCAGCGICACCCICCACCAIGCA 204
                                                                                                   Query Match 14.9%; Score 34.8; DB 61; Length 451; Best Local Similarity 55.9%; Pred. No. 3.8; Matches 66; Conservative 0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 451
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TMAGE:242137"
/clone="IPAGE:242137"
/tissue=Itpe="adenocarcinoma"
/lab_host="DH109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: -400P from Gibco
High quality sequence stop: 426.
Location/Qualifiers
1. 451
                                                                                                                                                                                                                                                                                                                                                  MRNA sequence.
A1829206
A1829206.1 GI:5449877
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FEATURES

A1010074/c LOCUS

DEFINITION

ACCESSION VERSION KEYWORDS

BASE COUNT ORIGIN

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0; Gaps

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1 (bases included to 597)

Souglas.S.E., Gallant,J.W., Bullerwell,C.E., Wolff,C.,
Munbolland,J. and Reith,M.E.
Winter flounder expressed sequence tags: Establishment of an EST database and identification of novel fish genes

In Marine Blotechnology (1999) In press
On May 18, 1998 this sequence version replaced gi:3136829.
Contact: Reith M Marine Biology
NRC Institute for Marine Biosciences
1411 Oxford St., Halifax, Nova Scotia, B3H 321, Canada
Tel: (902) 426-8276
Fax: (902) 426-8276
Fax: (902) 426-8413
Email: michael.reith@nc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pleuronectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AWU13553 597 bp mRNA EST 10-SEP-1999 LID02sk Winter flounder intestine Pleuronectes americanus CDNA AW013553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 AGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 33.2; DB 40; Length 292; 56.4%; Pred. No. 9.5; Live 0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 GCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGCA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pleuronectes americanus"
/db_xref="taxon:8263"
/clone='lip02sk"
/clone_lib="Winter flounder intestine"
/esx="female"
/dev_stage="adult"
                                                                                                                                     /clone_lib="Soares_testis_NHT"
                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1619724"
               High quality sequence stop: 225
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .597
                                                                                                                                                                             /lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pleuronectes americanus. Pleuronectes americanus
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Best Local S
Matches 62,
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ORIGIN
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AW013553/c
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          윱
                                                                                                                                                                                                                     /clone_lib="Lambda-PRL2"
/note="Vector: lambda 2ip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but acrial tissue (stems, flowers and
sliques. The vector is RRL's lambda Zip-Lox. The CDNA
inserts were directionally cloned with Sal-Not arms using
oligo dr primed CDNA.

121 c 130 g 153 t 10 others
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 292)
S NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
I Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergénih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Ennald, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA991822 292 bp mRNA EST 03-JUN-1998 ot45c07.sl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619724 3', mRNA sequence. AA991822.1 GI:3178704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 ITTICTGACAAATICCTCCTATGAGTCCAGCTICCTGGAATTGCTTGAAAAGCTCTGCCT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 CCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23; Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Indels
                                                                                                                        1. .545
/organism="Arabidopsis thaliana"
/strain="var columbia"
/db.xref="taxon:3702"
/clone="100A717"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg primer: -40ml3 fwd. Er from Amersham
Fax: 517-353-9168
Email: 22333cn@ibm.cl.msu.edu
Insert Length: 643 Std Exror: 0.00
Seg primer: T7 dye primer
High quality sequence stop: 369.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33.4; DB
Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.3%;
53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.67
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
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KEYWORDS
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AA991822/c
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ORIGIN
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Emsil: estewatson.wustl.edu
Contact David Sibley (toxoesteborcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
High quality sequence stop: 397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Alveolata; Apicomplexs; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                                                                                                                                                                          A1757641 490 bp mRNA EST 23-JUN-1999 ea33407.yl Eimeria 55-2 Sporozoite stage Eimeria tenella CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T., Martin, U., Wylle, T., Dewood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R. and
                                         208 CICANAIAAIAIAAACCIGIAIAITIAICICACAIIAAAGCAIAAIIICIIIAIIIIGAC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WashDrack Elmeria tenella project Unpublished (1999)
On Msy 9, 1996 this sequence version replaced gi:1132979.
On Msy 9, 1996 this sequence version replaced gi:1132979.
Contact: David sibley, Ph. D.
RashDrack Elmeria tenella project
WashDrack Elmeria tenella project
WashDrack Elmeria tenella project
WashDrack Park Parkway, Box 8501, St. Louis, MO 63108, USA 7el: 314 286 1810
Fax: 314 286 1810
Emsil: estëwatson.wustl.edu
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/organism="Eimeria tenella"
                                                                                                                                                                                                                                                                                                                                                                                         AI757641.1 GI:5151296
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eimeria tenella.
Eimeria tenella
                                                                                                                                         168 TCTCCCTT 175
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ORIGIN
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AI757641/c
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High Throughput Sequencing Center
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RFCI-11. For BAC
library availability, please contact pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Patter.1087 row: L column: 6
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Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 522)
Mahairss, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Reller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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m c} 64 g 178~{
m t} 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ718755 522 bp DNA GSS 13-JUL-1999

HS_5511_B2_F03_T7A RPCI-11 Human Male BAC Library Homo sapiens

genomic clone Plate=1087 Col=6 Row=L, genomic survey sequence.

AQ718755.1 GI:5468071
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/clone_11b="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                   182 CCAGCGTCACCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAAC 231
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13.9%; Score 32.6; DB 82; Length 5
Best Local Similarity 53.1%; Pred. No. 17;
Matches 68; Conservative 0; Mismatches 60; Indels
                                  4 others
                                                                                                                                                                    Indels
                                                                                                                                                                    48;
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                                                                                                                     / Mstch 14.2%; Score 33.2; D Local Similarity 56.4%; Pred. No. 12; nes 62; Conservative 0; Mismatches
                                  107
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/db_xref-"taxon:9606"
              /note="Organ: intestine"
167 c 166 g 10
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High quality sequence stop: 522.
Location/Qualifiers
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                                    153 a
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AQ718755
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13.8%; Score 32.4; DB 51; Length 490;
Best Local Similarity 54.1%; Pred. No. 19;
Matches 66; Conservative 0; Mismatches 56; Indels 0
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48 CTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGAC 107

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128 IGCIGCIGIIIGCACAICTICCIICAGCIGCIGGAIACGCICGGCAAICGCCIGGGCCIC 69
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²³² AC 233 | | 8 GC 7

Search completed: March 19, 2000, 08:56:37 Job time: 579 sec

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Query Match Matches

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WPI; 96-151776/16.
                                                                                                                                                                                                                     27-JUN-1994; CA-126787.
(PRED/) PREDDIE R E.
                                                                                                                                                                                                      27-JUN-1994; 126787
27-JUN-1994; CA-1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 936 BP;
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                                                                                                                     305 gagegécercagegécarecegagegérergégéceergergéaakcagégeegege 246
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                                                                                   6 GACTICAGIGICICCICCAICCCAGGAGCGCAGIGGCCACIAIGGGGICIGGGCIGCCCC 65
                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins and nucleic acids associated with Alzheimer's disease used to develop products for diagnosis of Alzheimer's disease and related conditions, hyperlipoproteinaemia or cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interacte countitions, inyperinpoproteinaemia of carolovascular disease claim 9: Fig 3A: 67pp: English.

2 Open reading frames (T18068 and T18069) identified in the apolipoprotein E (ApoE) antisense sequence code for proteins apolitoprotein E (ApoE) antisense sequence code for proteins apoEt4 (R02113) and apoEt41 (R92114), respectively. Both ORRs are transcribed from an upstream regulatory region (T18074) are transcribed from an upstream regulatory region (T18074) the significance of these and other sequences (see also T18055-77) in the actiology of Alzahlar's disease (AD) provides means for diagnosing AD and related diseases, for the design of therapeutic reagents (e.g. ribozymes or antibodies) and potentially for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.7%; Score 29; DB 1; Length 597; 54.1%; pred. No. 3.4; tive 0; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 CGGCCGCCACTGTGGGCTCCCTGGCCGCCAGCCGCTACAGGAGCGGG 197
                                                                                                                                                       66 TIGTCCTCCTCTTGACCCTCCTTGCAGCTCACATGGAACAGGGCCGGG 114
                                                                                                                                                                             DB 1; Length 936;
                                                                                                                                                                                                                                                                                                                                                Alberton disease, beta-amyloid peptide precursor; APP; antisense; hyperlipoproteinaemia; cardiovascular disease; gene therapy; apolipoprotein; ApoE4; ss.
                  // Match
12.7%; Score 29; DB 1; Length 936
Local Similarity 54.1%; Pred. No. 4;
nes 59; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 T;
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/*tag- a
/*tag- axept- pos:505. .507:_aa.Ala
/transl_except- pos:553. .555:_aa:Ser
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T18070/c
ID T18070 standard; cDNA; 936 BP.
                                                                                                                                                                                                                                                                  118068/c
ID T18068 standard; cDNA; 597 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-DEC-1995.
27-JUN-1994; 126787.
27-JUN-1994; CA-126787.
(PRED/) PREDDIE R E.
Bergmann JE, Preddie RE;
WPI: 96-151776/16.
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22-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                22-MAY-1996 (first entry)
Human ApoE4 cDNA.
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Homo saplens

CA2126787-A

Sequence

Ouery Match

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Proteins and nucleic acids associated with Alzheimer's disease - related conditions.

Trelated conditions, hyperilopproteinaemia or cardiovascular disease and used to develop products for diagnosis of Alzheimer's disease and used to conditions, hyperilopproteinaemia or cardiovascular disease claim 13; Pig 6A; 67pp; Engilsh.

2 open reading frames (T18068 and T18069) identified in the apolioporotein E (ApoE) antisease sequence code for proteins apoBLL (R2213) and apoBLL (R32114), respectively. Both OREs are transcribed from an upstream regulatory region (T18074).

C are transcribed from an upstream regulatory region (T18074) compline to form a hybrid ORE, ApoE4LLX (T18070).

C the significance of these and other sequences (see also T18065-77) in the actiology of Alzheimer's disease (AA) provides means for diagnosing AD and related diseases, for the design of therapeutic tengents (e.g. ribozymes or antibodies) and potentially for gene 305 GAGCGCGCCTCAGCGCCATCCGCGAGCGCCTGGGGGCCCTGGTGGAACAGGGCCGGTG 246 Gaps 6 GACTICAGIGICICCICCATCCCAGGAGCGCAGIGGCCACIAIGGGGICIGGGCIGCCCC 65 100-UN-1996 (first entry)
Human apolipoprotein-E (ApoE) CDNA.
Recombinant, human; apolipoprotein-E; ApoE; insect cells; larva;
Manduca sexta; human; apolipoprotein-E; ApoE; insect cells; larva;
haamolymph; lipid complex; biologically active; ds. ö 66 TIGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGG 114 ; DB 1; Length 936; 245 CGGCCGCCACTGTGGGCTCCCTGGCCGCCAGCCGCTACAGGAGCGGG 197 134 T; Human ApoE4Lx2 cDNA.
Alzheimer disease; beta-amyloid peptide precursor; APP;
antisense; hyperlipoproteinaemia; cardiovascular disease;
gene therapy; apolipoprotein; ApoE4Lx2; ss.
Homo sapiens.
Location/Qualifiers
cds
1. .597 50; Indels /*tag= a /transl_except= pos:505. .507:_aa:Ala /transl_except= pos:553. .555:_aa:Ser /transl_except= pos:553. .555:_aa:Ser 336 G; 05-DEC-1995. 04-UNH-1991; 709949. 04-UNH-1991; UG-709949. (WISC) WISCONSIN ALDMNI RES FOUND. Attle AD, Beckage NZ, Gretch DG, Sturley SL; WPI: 96-029812/03. 0; Mismatches Ouery Match
12.7%; Score 29;
Best Local Similarity 54.1%; Pred. No. .
Matches 59; Conservative 0; Mismatch T06957 standard; cDNA to mRNA; 1157 BP. 106957; 317 C; Location/Qualifiers 62. .119 /*tag= a note= "misc_signal" 62. .1015 Location/Qualifiers 1. .597 /*tag= a



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Prodn. of recombinant apo:lipoprotein E in insects - by infecting Handuca sexta larvae with recombinant Autographica californica and Handuca sexta larvae with recombinant Autographica californica or nuclear polyhedrosis baculovitus vector.

Profice of Columns 11-14; 10pp: English.

Recombinant human apolipoprotein-E (ApoE) (R86791) can be produced Recombinant human apolipoprotein-E (ApoE) (R86791) can be produced construct (confg. an ApoE-encoding sequence, by preparing a genetic construct (confg. an ApoE-encoding sequence of e.g. 106957, and flanking regulatory sequences enabling the protein conformation of the apolitical and an insect cells), which is then introduced into a conformation of conclear polyhedrosis virus) and recombinant Autographica californica hademolymph of the larval host. The ApoE produced is in a form chaemolymph of the larval host. The ApoE produced is in a form cannot be actieved in insect cell cultures, and can therefore be consed in therpeutic applications:

Sequence 1157 BP: 212 A; 370 C; 426 G; 149 T;
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0; Gaps

Ouery Match 12.7%; Score 29; DB 1; Length 1157; Best Local Similarity 54.1%; Pred. No. 4.3; Matches 59; Conservative 0; Mismatches 50; Indels

Search completed: March 20, 2000, 18:37:54 Job time: 8528 sec

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	A175764 A074026 T41535 T41523 A006274 A198136			10 136119 11 155181 11 155783 12 R34436 13 AA40444 13 AZ19495 50 AI692905
		2002488848999999999999999999999		
34.8 14.9 34.8 14.9 34.14.5 33.4 14.5 33.2 14.2 33.5 14.2	8 8 13. 1.8 8 13. 1.8 8 13.	24444444 24444444444444444444444444444	11	66 66 67 66 66 66 66 66 66 66 66 66 66 6
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AL IGNMENTS

AI857998 404 DP mRNA EST 26-AUG-1999 WJ69b01.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408041 3', mRNA sequence. AI857998.1 GI:5511614 EST.	Homo sapiens Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Bukheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 404)	NCI-CGAP http://www.ncob.nam.nam.yov/ncirgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Onpublished (1997)	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Tel: (301) 496-1550 Email: Robert_Strausberg@hih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDM Library Preparation: M. Bento Soares, Ph.D. Chan Library Praved by: Gred Lennon, Ph.D.	NA Sequencing by: Washington University Genome Sequencing Center of Sequencing Center of Sequencing NCI-CGAP clone distribution information can be trough the I.M.A.G.E. Consortium/LLML at:
RESULT 1 A1857998/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	ORGANISM	AUTHORS TITLE JOURNAL COMMENT		

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differentiated (4 pooled tumors, including primary and 59 CAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCT 118 0; Gaps Query Match
74.8%; Score 175; DB 61; Length 404;
Best Local Similarity 99.4%; Pred. No. 6.6e-41;
Matches 175; Conservative 0; Mismatches 1; Indeis Seq primer: -40UP from Gibco High quality sequence stop: 395. Location/Qualifiers 97 BASE COUNT ORIGIN FEATURES RESULT 셤 ð ò 셤

Bonaldo

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Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dr track served to identify it as a clone from the normalized
oligo-dr track served to identify it as a clone from the normalized
adult Lung ilbrary. CDNA Library Preparation: M. Fatima Bonaldo,
ph.D. Clone distribution: clones will be available through Research Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Euharyota; Metazoa; Chordata; Craniata; Murinae; Rattus.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 328)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene 451 Eckerdin Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8265 Fax: 319 335 9565 AI136523 328 bp mRNA EST 11-FEB-1999 UI-R-C2p-nq-e-02-0-UI.SI UI-R-C2p Rattus norvegicus CDNA Clone UI-R-C2p-nq-e-02-0-UI.3', mRNA sequence. AI136523.1 GI:3637300 On Jan 19, 1998 this sequence version replaced 91:2150222 Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa Genome Res. 6 (9), 791-806 (1996) Norway rat. VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION JOURNAL MEDLINE COMMENT REFERENCE AUTHORS TITLE AI136523/c ACCESSION

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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
Diversity of Washington
401 Queen Anne Avenue North, Sesttle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-ll. For BAC
Library availability, please contact Pieter de Jong
(pleter@dejong.med.buffal.o.edu).Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
plate: 1087 row: L column: 18
Seq primer: T7
Class: BAC ends
                      (eller, A., Shsker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

U Upublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1402231.
Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550

Email: Robert Strausbergenih.gov
This Glone is available royalty-free through LiNL; contact the IMAGE Consortium (info@image.linl.gov) for further information.
Insert Length: 891 Std Error: 0.00
Seq primer: -41m13 fwd. Er from Amersham
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2889a03.81 NCI_CGAP_GCB1 Homo sspiens cDNA clone IMAGE:704620 3',
                                                                  Sequence-tagged connectors: A sequence spproach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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/lab_host="wettor: pr773D-pac (Pharmacia) with a modified
polylinker; site_1: Not I; Site_2: Eco Ri; The UI-R-C2p
library is a subtracted library derived from the U-R-C1
library, which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
the mixture. The subtracted library of origin of a clone within
constructed as follows: PCR amplified obna inserts from
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remaining single-stranded circles and electroporated
UI-R-C2P library in the form of single-stranded circles and electroporated
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 552)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
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HS_5511_B2_F09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1087 Col-18 Row-L, genomic survey sequence.
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                                                                                                                     /strain="Sprague-Dawley"
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##experimental_source strain AB972 GENETICS

##experimental_source strain AB972 GENETICS #GENETICS #GENETICS SGD:GCD6 ##arcos_references SGD:S0002619; MIPS:YDR211w #map_position 4R KEXWORD5 #Instalation regulation GURTY GURTY GURTY GURTY GURTY MATCh ##arches ##arch	RESULT 4 JC5237 #type complete ENTRY OSMOCIA-like protein precursor · tomato TILLE OSMOCIA-like protein precursor · tomato ORGANISM #formal_name_Lycopersicon esculentum #common_name tomato DRTE 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change	rence A Gebook	;; PID:g122053 ent and play pathogens. rtatus predict	MMARY Ouery Best L Matche	RESULT 5 S73757 *type complete ENTRY hypothetical protein Fil_orf879 - Mycoplasma pneumoniae (ATCC 711LE 29342) (SGC3) ORGANISM *formal_name Mycoplasma pneumoniae *variety ATCC 29342 DATE 27-Feb-1997 *sequence_revision 25-Apr-1997 *text_change	ACCESSIONS S7375 REFERENCE \$73327 REFERENCE #Immelectch, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Hermann, R. B.C.; Hermann, R
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j.

the WORMPEP database can be found at the WORMPEP database can be found at the WORMPEP database can be found at the tp://www.aspara.ca.u/kProjects/Calegoun/wormpep This sequence was speara to the part of batterial clone conting of human chormosome 1. Constructed by the Singer Centre Chromosome 1. Mapping Croup. Turners in the 11Dray Red-1. Constructed at the Roswell Review of the 11Dray Red-1. Constructed at the Roswell Review of the 11Dray Red-1. Constructed at the Roswell Review of the 11Dray Red-1. Constructed at the Roswell Review of the 11Dray Red-1. Constructed the 12Dray Red-1. Constructed the	who sp. Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Eukaryota; Metazoa; Chordata; Vertebrata; Mus. Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3626) Kubota,Y. Kubota,Y. Direct Submission Submitted (26-JUL-1996) to the DDBJ/EMBL/GenBank databases. Yasue
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		<i>J.</i>

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Tequests: clonerequest@sanger.ac.uk

On Jul 27, 1999 this sequence version replaced gi:5579004.

On Jul 27, 1999 this sequence exerations:
Furing sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations annotation name. Note that the together with a note of the overlapping clone, as we submit sequence submission variation annotation may not be found in the sequence submission.

The following abbreviations are used to associate primary accession rumbers given in the feature table with their source databases: numbers given in the feature table with their source databases: numbers given in the feature table with their source databases: numbers given in the feature table with their source databases on the WORMPEP; Information has been finished according to sequence map criteria as follows. An has been finished according to sequence map criteria as follows. An has been finished according to sequence map criteria as follows. An extempt 1s made to resolve all sequencing problems, such as attempt and repeats, but not necessarily within known compressions and repeats, but not necessarily within known sequence agequence thements (e.g. Alu). Where the sequence sequence is an annotation using the 'unsure' sequence as an annotation using the 'unsure' sequence and annotation and the 'unsure' sequence and annotation and the 'unsure' sequence and annotation and the 'unsure' sequence and annotation using the 'unsure' sequence and annotation and the 'unsure' sequence and annotation and the 'unsure' sequence and annotation and the 'unsure' sequence a
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                            Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 36676)
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1. 36676
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                                     ORGANISM
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SPRYGPDILGRLVKYLQVVGMFASTYLLLIMSLDRCLAICQPLRSLRRRTDRLAVLAT
WLGCLVASVPQVHIFSLREVADGVFDCWAVFIQPWGPKAYVTWITLAVTYVPVIVLAA
CYGLISFKIWQNLRLKTAAAAAAAEGSDAAGGAGRAALARVSSVKLISKAKIRTVKMT
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    Kubota, Osaka University Medical School, Department of Obstetrics and Gynecology; 2-2 Yamadaoka, Suita, Osaka 565, Japan (E-mail:Kubota@gyne.med.osaka-u.ac.jp, Tel:81-6-879-3351, Fax:81-6-879-3359)
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                                                                                                                                                                                                                                                                                                                                                                           Kubota.Y.', Kimura.T., Hashimoto.K., Tokugawa.Y., Nobunaga.K.,
Azuma.C., Saji.F. and Murata.Y.
Structure and expression of the mouse oxytocin receptor gene
Structure and expression of the form of the mouse oxytocin receptor gene
97179034
                                                                                                                                                                     (hoses i to 3626)

(bases i to 3626)

Kubota, Y., Sali, F. and Murata, Y.

Structure and Expression of the Mouse Oxytocin Receptor Gene Unpublished (1996)
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/cell_type-"ES cell"
1. 1530
1531. .1798
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/strain-"1295V"
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1799. .2240
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Matches 57; Conservative
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RESULT 14 HSJ858B16 LOCUS DEFINITION

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BASE COUNT ORIGIN

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MEDLINE FEATURES TITLE JOURNAL

TITLE JOURNAL REPERENCE AUTHORS

intron

exon

intron

exon



GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model Run on: March 21, 2000, 14:42:21 ; Search time 479.47 Seconds (Without alignments) -1139.903 Million cell updates/sec

Title:

Perfect score: 180
Sequence: 1 CAGGAGGGCGAGTGGCCACTA......CTTGAAAAGCTCTGCCTCT 180
Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database : GenEmb1:*

Word size : 0

Number of hits that pass the threshold : 164:

1642386	
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threshold	*****
pass the gdb_bal:* gdb_bal:* gdb_bal:* gdb_pat:* gdb_ph:* em_ph:* em_ph	gb_htg3 gb_htg4 gb_htg5 gb_htg7 em_htg1 em_htg3 em_htg3
Lb and	444444444
Hits	

50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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& Query e Match Length	.8 50.4 192650	.8 50.4 200000	4 18.6 97580	.2 17.9 36676	.2 17.3 177241	.2 17.3 303319	11.2 97339	.8 17.1 5280	8 17.1 168986	8 17.1 110000	.8 I/.1 I/9622	14 TO:9 TO9T	4 16 9 1098	4 16.9 1669	4 16.9 1131	.4 16.9 1206	.2 16.8 2803	0 16.7 751	0 16.7 85109	0 16.7 4341	0 16.7 124990	30 16.7 159125	10.0	16.6	.8 16.6	.6 16.4	.6 16.4	. 6 16.4	.6 16.4	0.0	10.4	* C T C -	10.3	.4 TO.3	16.3	10.3	.4 16.3	.4 16.3	.4 16.3	.4 Ib.3	.4 L0.3	7.01 7.
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ALIGNMENTS

ABOUT 1 ABO13048 115 LOCUS ABO23048 115 DEFINITION Homo saplens clone:5319, clone:5319, version ABO23048 VERSION ABO23048 10 KEYMORDS HTG. SOURCE Homo saplens OKCANISM Homo saplens	AB023048 192650 bp DNA Homo sapiens genomic DNA, chrocione:53L9, complete sequence. AB023048	AB023048 192650 bp DNA Chromosome 6p21.3, 16mo sapiens genomic DNA, chromosome 6p21.3, 180023048 Complete sequence. AB023048.1 G1:5672603 HFTG. HFTG. HOMO sapiens cell_line:9785K DNA, clone:53L9. Homo sapiens	PRI 6p21.3, HLA ne:53L9.	AB023048 192650 bp DNA PRI 20-NOV-1999 Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region, conce:5319, complete sequence. AB023048 AB023048.1 GI:5672603 HFTG. HOMO sapiens cell_line:9788K DNA, clone:5319.	
Eukaryota; Eutheria;	Metazoa; Ch Primates; Ca	Eukaryota; Metazoa; Chordata; Craniata; Vertebra† Eutheria; Primates; Catarrhini; Hominidae; Homo.	a; Vertebrat idae; Homo.	a; Mammalia;	
	ns Metazoa; Ch	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	a; Vertebrat	a; Mammalia;	
	ns cell_line	::978SK DNA, clo	ne:53L9.		
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clone:53L9	, complete s	ednence.			
	ns genomic D	NA, chromosome	6p21.3, HLA	class I region,	
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project of JST
Japan Science and Technology Corporation (JST)
Japan Science and Technology Corporation (JST)
Japan Science and Technology Corporation Japan
For further information about this sequences, please visit our
sequence archive Web site (http://www-alls.tokyo.jst.go.jp/HGS/top.
html) or send email to webmaster@www-alls.tokyo.jst.go.jp.
Location/Qualifiers
J. 200000
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/standard_name="D651851"
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Homo sapiens clone UWGC:370M23.002 from 6p21, complete sequence.
AC005937
AC005937.1 GI:3845393
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/note="SHGC-3064; The location
site of PCR primers."
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/note="UT5233;The location is
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47531 c 49366 g 50498
                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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KEYWORDS
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S Shilas, 7. Taniya.G. Oka.A. and Inoko.H.

Homo sapiens 2,229,818bp genomic DNA of 6p21.3 HLA class I region

L Published Only in Database (1999) In press

E 2 (bases I to 200000)

S Hirakawa.M. Yamaguchi.H., Imai.K. and Shimada.J.

Direct Submission

L Submitted (21.SEP-1999) to the DDBJ/EMBL/GenBank databases. Mika

Hirakawa. Japan Science and Technology Corporation (JST), Advanced

Databases Department; 5-3, Yonbancho, Chiyoda.ku, Tokyo 102-0081,

Japan (E-mail:mikatokyo.jst.go.jp,

URL:http://www.alls.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
                    Shihmarr., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahram,S. and Inoko,H.,
Wolecular dynamics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp HiA class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (29-JAN-1999) to the DDBJ/EMBL/GenBank databases. Takashi
Shilna, Tokai University School of Medicine, Department of
Molecular Life Science 2; Bohseidai, Isehara, Kanagawa 259-1193,
Japan (E-mail:tshilna@is.iCc.u-tokai.ac.jp, Tel:81-463-93-1121,
Fax:81-463-94-8884)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Phone:+81-463-93-1121, Fax:+81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 50.4%; Score 90.8; DB 10; Length 192650; Best Local Similarity 97.9%; Pred. No. 3.6e-19; Matches 92; Conservative 0; Mismatches 2; Indels 0;
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1. 192650
7. Grganism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="978SK"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 192650)
Shiina, T. and Takishima, N.
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AP000511.1 GI:5926698
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/map="6p21.3"
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/note-"clonal variation with 3' overlapping clone"
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/note="clonal variation with 3' overlapping clone insertion of 17bp repeat" a 11489 c 12284 g 11994 t
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                                                                             /sub_clone="UWGC:370M23.002"
/clone_lib="Research Genetics BAC Library"
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286. .7584
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/rpt_family-"Alu"
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39583. 40010
39583. 40010
40046. 40156. 40156
43194. 43372
/rpt_family="MER5"
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11295. .31594
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34223. 34290
/rpt_family="MIR"
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/rpt_family="Alu"
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/rpt_family="Alu"
complement(6972. .
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5510, .25802
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Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.
HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrsp assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part
of this entry's ASN.1 file.
                                                                                                                                  Large scale sequence analysis of the human MHC class I region
Unpublished (1998)
                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                           1 (bases 1 to 47323)
Janer, H., Guillaudeux, F., Vu, O., Kutyavin, T., Harter, H. and
Geraghity, D.
                                                                                                                                                                                                                                                                                                         University of
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                                                                                                                                                                Fred Hutchinson Cancer Research Center
The Clinical Research Division
The Clinical Research Division
The Clinical Research Division
Seattle, WA 98109-1024
2 (bases 1 to 47323)
Geraghty,D.E. and Olson,M.V.
Geraghty,D.E. and Olson,M.V.
Submitted (05-NOV-1998) Human Genome Center, University Washington, Box 352145, Seattle, WA 98195, USA
University of Mashington Human Genome Center
Box 352145 Seattle, WA 98195
Contact: Daniel E. Geraghty (geraghty@fhorc.org)
Overlapping Sequences:
5: UWGC:370m23.013 (Genbank Accession: AC005530)
3: UWGC:370m23.012 (Genbank Accession: AC004211)
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9209. 9505

/note-"Alusg repeat: matches 1. .295 of consensus"

11780. 12007

/note-"LiMil repeat: matches 5465. .5691 of consensus"

12018. 12387

/note-"HENY23 repeat: matches 1184. .1573 of consensus"

12454. .12843

/note-"LiMil repeat: matches 5679. .5763 of consensus"

/note-"Alubb repeat: matches 1. .297 of consensus"

/note-"Alubb repeat: matches 5763. .6159 of consensus"
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/mote="Aludo repeat: matches 1. .136 of consensus" 1346. .13573
/mote="Aluds/x repeat: matches 96. .293 of consensus" 13625. .13924
/mote="Aluds/x repeat: matches 1. .301 of consensus" 13936. .14230
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/mote="Mix repeat: matches 11. .261 of consensus" 14739. .14785
/mote="Mix repeat: matches 2370. .261 of consensus" 15147. .15467
/mote="Linki repeat: matches 2370. .2690 of consensus" 15147. .15467
/mote="Mix repeat: matches 1. .296 of consensus" 1600. .16300
/mote="Aludsy repeat: matches 1. .291 of consensus" 1600. .16300
/mote="Aludsy repeat: matches 1. .291 of consensus" 16422. .16732
/mote="Aludsy repeat: matches 1. .311 of consensus" 16422. .16732
                            'note-"AluJ/FRAM repeat: matches 217. .294 of consensus'
                                                                                                                                                                                                                                                                                                                                                            .255. .1501
note="AluJo repeat: matches 12. .282 of consensus"
                                                                                                                                                                                                                 .869. .2134
.note="AluJb repeat: matches 21. .275 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          16733, .16813
/note="L2 repeat: matches 2667. .2746 of consensus"
complement(16814. .17293)
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Anote-"Ashusc repeat: matches 4. .295 of consensus"
4054. 5144
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/hote-Alusx repeat: matches 1. 299 of consensus"
8457. 8776
/hote-Alux repeat: matches 1. 311 of consensus"
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note-"AluJb repeat: matches 1. .307 of consensus"
                                                                          note-"match: GSSs AQ377982 AQ380087"
6907. .17100
bote-"MIR repeat: matches 2. .197 of consensus"
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/note="38 copies 2 mer tt 78% conserved"
18540. .19522
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Lutter Submission

Submission

CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

CB10 11, 1999 this sequence version replaced gi:4014529.

During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations

Variation anotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences

only a small overlap as described above.

The following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

Em; EMB1; Sw; SWISSPROT; Tr; TRENEL

This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems,

such as compressions and repeats, but not necessarily within known

sequence is ambiguous, there is an annotation using the 'unsure'

meature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 human chromosome 22, constructed by the Sanger Centre Chromosome 22 http://www.sanger.ac.uk/MED/Chr22
SJN18 is from the library RPCI4 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: prPRAC2
IMPORTANT: This sequence is not the entire insert of clone 591N18.
It may be shorter because we arrange for a small overlap between neighbouring submissions.
The true left end of clone 229A8 (186090) is at 97475 in this sequence. The true right end of clone 129A8 (186090) is at 97475 in this sequence.
  ö
                                                                                                                                                                                                                                                                                                      HS591N18 97580 bp DNA PRI 23-NOV-1999 UMA Bund DNA sequence from clone 591N18 on chromosome 23613.1-313.2 Contains a COXOB (Cytochrome C Oxidase subunit VID (EC 1.9.3.1)) pseudogene, ESTs, GSSs and two putative CpG islands, complete
                                                                          78 CAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAGTTCCTCCT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primetes; Catarrhini; Hominidae; Homo.
1 (bases 1 to 97580)
Steward,C.
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  ö
     Indels
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HTG; COX6B; CpG Island; Cytochrome C Oxidase.
  5
                                                                                                                                  Mismatches
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/db_xref="taxon:9606"
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/clone="RP4-591N18"
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  Conservative
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VERSION
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Matches
                                                                                                                                                                                                                                                          RESULT HS591N18
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Anote-"SYA repeat: matches 521. 954 of consensus"
20019. .2036
Anote-"SYA repeat: matches 521. 954 of consensus"
Anote-"SYA repeat: matches 519. 994 of consensus"
Anote-"SYA repeat: matches 519. 994 of consensus"
Complement(20855. 20945)
Anote-"Alusx repeat: matches 1. 165 of consensus"
Anote-"Alusx repeat: matches 1. 162 of consensus"
Anote-"Alusx repeat: matches 1. .367 of consensus"
Anote-"FRAM repeat: matches 1. .365 of consensus"
Anote-"FRAM repeat: matches 1. .365 of consensus"
Anote-"Aluxb repeat: matches 1. .365 of consensus"
Anote-"Aluxb repeat: matches 1. .307 of consensus"
Anote-"Alux repeat: matches 2. .311 of consensus"
Anote-"Alux repeat: matches 2. .311 of consensus"
Anote-"Alux repeat: matches 1. .133 of consensus"
Anote-"Alux repeat: matches 1. .133 of consensus"
Anote-"Alux repeat: matches 103 .206 of consensus"
Anote-"Alux repeat: matches 1. .131 of consensus"
Anote-"Alux repeat: matches 1. .118 of consensus"
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/note="SVA repeat: matches 2. .954 of consensus"
19061. .20976
/note="Tandem repeat. Some base discrepancies edited.
Assembly is consistent with Restriction Digest."
19115. .20959
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32623 .32927
//note="AluJb repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
                                                                                                                                                                                                                                              'note="CpG island"
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                                                                                                                                                                                                                                                                                                   60.TIGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTT 119
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                 Query Match 18.6%; Score 33.4; DB 11; Length 97580; Best Local Similarity 57.0%; Pred. No. 1.6; Matches 61; Conservative 0; Mismatches 46; Indels 0;
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/note="match: ESTs: Em:R53362 Em:278408 Em:AA521233...

MRNA

gene CDS

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Complement(join(16160. 17505.1822. .18382,18665. 18811, 19003. .19141,19318. .1954,21353. .21518,23432. .23685, 28473. .28484)

19003. .19141,19318. .19554,21353. .21518,23432. .23685, 28473. .28484)

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/note="fals8816.2"

Em:AA260704 Em:081215 Em:AB05121 Em:AA16640

Em:AA32493 Em:AA68312 Em:AA10955 Em:AA16640

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Em:AA717291 Em:AA32672 Em:AA005550 Em:AA290268

Em:AA717291 Em:AA2977 Em:AA005550 Em:AA290268

Em:AA717291 Em:AA2977 Em:AA297706 Em:AA290268

Em:AA61577 Em:AA29775 Em:AA10776 Em:AA63369

Em:AA61577 Em:AA297159 Em:AA10776 Em:AA63369

Em:AA071231 Em:AA297159 Em:AA10746 Em:AA63369

Em:AA071234 Em:AA297159 Em:AA10749 Em:AA59386

Em:AA971234 Em:AA097159 Em:AA10749 Em:AA593345 Em:H93993

Em:AA971234 Em:AA097159 Em:AA10749 Em:AA593086

Em:AA971234 Em:AA09715 Em:AA10740 Em:AA553345 Em:H93993

Em:AA097124 Em:AA0087 Em:AA10740 Em:AA553345 Em:AA300851

Em:AA07744 Em:AA10482 Em:AA004124 Em:H9339 Em:AA300851

Em:AA77974 Em:AA10404 Em:AA297086 Em:AA59740 Em:AA107842

Em:AA77974 Em:AA10409 Em:AA595561 Em:H9339 Em:AA30871

Em:AA77974 Em:AA28551 Em:AA59440 Em:AA50871 Em:A18871

Em:AA77974 Em:AA2852 Em:AA29764 Em:AA99440 Em:AA300371 Em:AA36942 Em:AA39943 Em:AA36942 Em:AA39944 Em:AA36942 Em:AA39944 Em:AA36942 Em:AA39944 Em:AA36944 Em:AA36944 Em:AA36942 Em:AA36944 E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6985 .7081 .295 of consensus" /note="frage" matches 1. .295 of consensus" /note="frage" repeat: matches 1. .100 of consensus" /note="MIR repeat: matches 82. .255 of consensus" /note="MIR repeat: matches 9766. 10068 /note="MIR repeat: matches 1 ... 10069. .10004
                                                                                                                                                                                                                                                                                                                                                            4650. .4754
forte-"Alusg/x repeat: matches 200. .307 of consensus"
4990. .5281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 TGCCCCTTGTCCTCCTCTTGACCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA 92
             /gene-"dJ858B16.1"
/note-"match: GSS: Em:AQ545234"
3250. 3536
3640. 3836
3634. 3836
/note-"L2 repeat: matches 2497. .2701 of consensus"
                                                                                                                                                                                                                                                                         4356. .4646 /
/note="AluSx repeat: matches 21. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5806. 6231

/note-*MITIC repeat: matches 6. .460 of consensus"

/note-*FRAM repeat: matches 1. .140 of consensus"

6671. .6966

/note-*Alux repeat: matches 1. .295 of consensus"

/note-*Alux repeat: matches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 46. .208 of consensus" 13063. .13779
/note="L2 repeat: matches 1570. .2750 of consensus" 15018. .15404
/note="Alusy repeat: matches 1. .295 of consensus" complement(16160)
                                                                                                                                                                                                                                                                                                                                                                                                                                                4990. .5281
/note="AluSx repeat: matches 1. .292 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="14 copies 2 mer ta 100% conserved"
10104. 10399
/note="AluJb repeat: matches 1. .293 of consensus"
1099. .12289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.9%; Score 32.2; DB 11; Length 36676; ilarity 63.6%; Pred. No. 3.9; Conservative 0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene-"dJ858B16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /widence=not_experimental
/product="40488B16.1.1 (KIAA0542 (isoform 1))"
join(<273 * 454,1413 * 1488.1988 * 2073,2538 * .2614,
join(<273 * 454,1413 * 11488.1988 * 2073,2538 * .2614,
join(<273 * 11199,11271 * 12948,14414 * .14546,14669 * .14747,
11023 * .11199,11271 * .12948,14414 * .14546,14669 * .14747,
15784 * .15895,15983 * .16218)
/gene="4058B16.1" | /note="match: cDNAs: Em:AB011114" | /witchcc=not_experimental
/product="4058B16.1.2 (KIAA0542 (isoform 2))" | /product="4058B16.1.2 (KIAA0542 (isoform 2))" | /product="4058B16.1" | /product="405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPGPEDQEVEQOVQKELEQVEMQIQLIAEELQAQRQPIGACVARIQALRQALC"

join(<273. 494,1413. 1488,1978. 2073,2538. 2614,

3997. 4099,5606. 5702,8812. 8972,9435. 9509,10811. 10885,

11023. 11199,11271. 11528)
Em: R53964 Em: A1806913 Em: AA158770 Em: AA636285 Em: AA974403
Em: AA69535 Em: AA686196 Em: AA45626 Em: R51102 Em: AA562394
Em: AA6829554 Em: AA55345 Em: AA686685 Em: R51102 Em: AA682394
Em: AA971234 Em: AA55345 Em: A141022 Em: AA4159572 Em: A1361548
Em: AA971234 Em: R54651 Em: A141022 Em: AA159572 Em: A1361548
Em: AA971234 Em: R54651 Em: AA141022 Em: AA179744 Em: N64034
Em: AA595561 Em: AA086219 Em: A266102 Em: A1222370
Em: AA595561 Em: AA086219 Em: A7252377 Em: A1044249
Em: AA595561 Em: A1190893 Em: A1120375 Em: A170152
Em: AA67371 Em: A1190893 Em: A104075 Em: R546447 Em: A1126154
Em: AA67371 Em: A1190893 Em: A1042072 Em: R54647 Em: A1126154
Em: AA149582 Em: A310173 Em: A142072 Em: R54647 Em: A1126154
Em: AA16981 Em: A1192647 Em: A163324 Em: A1192647 Em: A1192647 Em: A1192647 Em: A1192647 Em: A1192647 Em: A1083921"
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/product="dd85816.1.2 (KIAA0542 (1soform 2))"
/protein_id="cla85.039.1"
/db_xref="61:5921490"
/translation="QAILHARENGLITRSWFWHQQAARROGOEWOTVACAHHRHGRL
KRAFCLMRESAQGLITREPTGREVAAEPHWAQLIZRAWRQWRECIALRGAERGKLMRAD
LHENGHSYLHRALQAWYTYOGRYRSILARSVARESQHINGOLIRGALRRWRENTMRAVDE
AKKTFQASTHYRRIICSRYLVQWREAVSVQMYYRQGDCAIWEAQKVLDRGCLRTWFQ
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RLSRTCROWRQDLAARQDSRATVRALWFVAFSLQAKWAYWLAFVLERRRKKARLQ
WALORYGGLLQEGATRLLRFAASMKASRQQLQAQQQVQAAHSLHRAVRRCATLWKQK
VLGRGGRPQPLAALAPSRKVTFEGPLLNRIAAGAGDGTLETKRPQASRPLGALGRLAA
EEPHALEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620. .913
/note="Alusx repeat: matches 1. .294 of consensus"
1444. .1687
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CDS

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note="AluSg/x repeat: matches 133. .302 of consensus"
23375. .23514
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18096. .18300
/note="MRR46C repeat: matches 113. .337 of consensus"
18366. .18558
/note="MIR repeat: matches 32. .247 of consensus"
18590. .18727
                                                                                                                                                                                                                                                                                                                                                                                                                      9543. .9847
/note="Aluy repeat: matches 30. .150 of consensus"
/note="Aluy repeat: matches 1. .303 of consensus"
9848. .10020
/note="Aluyo repeat: matches 150. .306 of consensus"
/note="Aluyo repeat: matches 150. .306 of consensus"
/note="Aluyo repeat: matches 1 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="FRAM repeat: matches -7. .168 of consensus" 23699. .24482
/note="L1 repeat: matches 2915. .3769 of consensus":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="LTR45 repeat: matches 389, .525 of consensus"
20657. .20771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="1.1 repeat: matches 3780. .3926 of consensus"
23516. .23691
                                                                                                                                                                                                                                                                                    6853. 7155
//note="Alur repeat: matches 1. .303 of consensus"
7218. 7516
/note="Alurb8 repeat: matches 1. .318 of consensus"
9018. 3309
//note="Alux repeat: matches 1. .294 of consensus"
9427. 9542
                                                                                                                                                                                                                                                                                                                                                                                                                    9427. .9542
//note="Aluyo repeat: matches 30. .150 of consensus"
9543. .9847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11227. .11641

//note="MER4C repeat: matches 22. .461 of consensus"

11642-.11957

//note-aluY repeat: matches 1. .310 of consensus"

11958-.11981
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21328. .21889
Anote-"MRE54B repeat: matches 1. .638 of consensus"
21958. .22115
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3218, .23373
                                                                                                                                                                                    6305. .6592
/note="AluJo repeat: matches 29. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1 repeat: matches 3975. .4613 of consensus"
22938. .23151
                                                     .2643 of consensus"
                                                                                                              5044. .5270
//note="Aluub repeat: matches 77. .303 of consensus" 6305. .6592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"L1 repeat: matches 4613. .4770 of consensus"
22116. .22245
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22246. .22887
                                                                                                  'note="MER1A repeat: matches 31. .527 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"AluSx repeat: matches 51. .295 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16411. 16616
Mote-*Alur repeat: matches 91. 296 of consensus"
16816. 17110
note-"AluSp repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="FRAM repeat: matches 1. .166 of consensus" (3152, .23217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 2. .297 of consensus"
                                                                                                                                                                                                           6404. .6907 --row. maccnes 29. .308 of c
/note="match: GSS AQ475194 clone 2579L10"
6853. .7155
                                                  repeat: matches 2630.
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10804. .11101
/note="AluSg re
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Direct Submission

Direct Submission

Submitted (26-JUL-1999) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, Uw. E-mail enquiries: hunqueryssanger.ac.uk Clone
requests: clonerquest@sanger.ac.uk

On Jun 29, 1999 this sequence version replaced gl:552835,

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

orresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:

Em: FEML: W.: SWISSPROT: TT:, TREMBL

This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 human chromosome 22, constructed by the Sanger Centre Chromosome 22 http://www.sanger.ac.uk/RGP/Chr22
402611 is from the 11brary RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jons For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCrPAC2 This sequence is the entire insert of clone 402611. The true right end of clone 232217 is at 56734 in this sequence. The true right end of clone 89814 is at 23403 in this sequence. The true right end of clone 600024 is at 96013 in this sequence.

Location/Qualifiers
                                                                                                                                                                 HS402G11 177241 bp DNA PRI 23-NOV-1999
Human DNA sequence from clone 402G11 on chromosome 22q13.31-13.33
Contains genes for SAPK3 (stress-activated protein kinase 3),
PRKM11 (protein kinase mitogen-activated 11), KIAA0315, ESTS, GSS
AL022328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2504. 2574
/note-"MERS0 repeat: matches 170. .243 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177241)
Coville,G.
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//hote="L2 repeat: matches 2643. .2747 of consensus"
2775. .3072
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/note="AluSg repeat: matches 1. .310 of consensus"
1373. .1659
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note="Alusq repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135. .447
note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSx repeat: matches 1. .298 of consensus"
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/db_xref="taxon:9606"
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                            Db 14533 ACTTTCAACTGCAGGTG 14549
93 CITIGCAACIGAAGCIG 109
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HS402G11/C
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3450. 33037
/note="rmax repeat: matches 1. 175 of consensus"
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34781. 34916
/note="4 copies 34 mer 87% conserved"
34792. 34910
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/note="7 copies 17 mer 74% conserved"
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Anote "LIMC/D repeat: matches 4184. 4755 of consensus" 32908. 33208 anote matches 1. 301 of consensus"
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33468. .33637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /D repeat: matches 4762. .5325 of consensus"
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hote="LIMEc repeat: matches 1501. .1751 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35932. 36042. "matches 2643. .2750 of consensus" 20532. 37622. 37622. "atches 255. .1397 of consensus" 37623. 37653
                                   24978. .25194

//note="LiMEc repeat: matches 272. .492 of consensus"

25933. .26246

//note="Aluy repeat: matches 1. .309 of consensus"

27926. .28225
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/note="AluSx repeat: matches 2. 302 of consensus" 28694 28997
/note="AluSy repeat: matches 1. 304 of consensus"
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/note="AluY repeat: matches 1. .303 of consensus"
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/note="LIMC/D
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7706. .37865
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ö ch 17.3%; Score 31.2; DB 11; Length 177241; 1 Similarity 57.0%; Pred. No. 8.7; 57; Conservative 0; Mismatches 43; Indels 0; Gaps 16 CACTATGGGGTCTGGGCTGCCCCTTGTCCTCTTGACCCTCGTTGGCAGCTCACATGG 75 Best Local Similarity Matches 57; Conserv Query Match ð

Db 109618 AACAIGGCIGGGGIGGACIGCAGGGAIGGAGCIGGGGCAG 109579 76 AACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAG 115 å

Db 109678 CACCAGGCTGCCCCAGCGGCTCCTCCCGGCCTTCTGCAGCCCCATCGCCCACATGG 109619

16617: 17335: 17992: 18287:

Lorders 1 to 30313)

Murny, D.M., Adams.C., Balley, M., Barbarla, J., Blankenburg, K., Bodeta, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Burkett, C., Burrows, J., Carter, M., Checko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Dupan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraquto, D., Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, L.L., Guevara, W., Raris, R., Hennandez, J., Rorden, J., Dines, M., Marlin, K., Marlinerz, C., Hosak, H., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Kong, Y., Koyar, C., Lu, J., Lucter, R., Marlinez, C., Morgan, M., Morris, M., Marlinez, C., Morgan, M., Morris, M., Marlinez, C., Morgan, M., Morris, M., Marlinez, C., Morgan, M., Morris, R., Marlinez, C., Morgan, M., Morris, S., Ray, D., Shah, E., Shah, E., Shah, R., Shan, M., Samuel, S., Say, J., Scherers, S., Shah, E., Shah, R., Shan, S., Ray, S., Shan, S., Ray, S., Shan, S., Ray, S., Shan, S., AC006927 303319 bp DNA HTG 21-027-1999 Homo sapiens chromosome 12p13.1-17.1-21.3 clone RPCIl1-444721, *** SEQUENCING IN PROGRESS ***, 139 unordered pieces. Worley, K.C.

Direct Submitsation

Submitted (26-FEB-1999) Molecular and Human Genetics, Baylor

College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Oct 21, 1999 this sequence version replaced g1:5887346

* NOME: This is a "working draft' sequence. It currently

* consists of 139 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 303319) 830: contig of 830 bp in length 1660: contig of 830 bp in length 2498: contig of 838 bp in length 3378: contig of 838 bp in length 4616: contig of 878 bp in length 4616: contig of 787 bp in length 6430: contig of 877 bp in length 6330: contig of 877 bp in length 6330: contig of 872 bp in length 6411: contig of 1011 bp in length 6411: contig of 727 bp in length 1020: contig of 805 bp in length 1171: contig of 734 bp in length 1172: contig of 734 bp in length 1173: contig of 734 bp in length 1173: contig of 734 bp in length 1173: contig of 735 bp in length 1335: contig of 737 bp in length 1335: contig of 578 bp in length AC006927.19 GI:6091655 HTG; HTGS_PHASE1. Unpublished 2 (bases 1 to 303319) 9411: 10220: 11025: 11817: 12571: 13368: 14228: 15013: Homo saplens RESULT 7
AC006927
LOCUS
DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS COMMENT

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1888 20055 CONTIG OF 668 bm leagth 20055 20155 CONTIG OF 658 bm leagth 20155 20155 20155 CONTIG OF 704 bm leagth 20155 CONTIG
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DD 98830 TATAGCCCTTCTCAGCATCACAGATGGCACATGCCAGGACAGGCCTGGCAGCTGCTGA 98889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC011039 97339 bp DNA HTG 07-DEC-1999
Homo sapiens clone RP11-7H18, LOW-PASS SEQUENCE SAMPLING.
AC011039
AC011039.2 GI:6532109
HTG: HTGS_PHASE0.
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contig of 737 bp in length
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contig of 1253 bp in length
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contig of 650 bp in length
contig of 157 bp in length
contig of 1053 bp in length
contig of 1063 bp in length
contig of 1002 bp in length
contig of 1003 bp in length
contig of 1238 bp in length
contig of 1235 bp in length
contig of 1338 bp in length
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contig of 1344 bp in length
contig of 2473 bp in length
contig of 5478 bp in length
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contig of 36022 bp in length
contig of 36032 bp in length
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67345 c 67086 g 86209 t

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    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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* 10551 11434: contig of 884 bp in length * 11435 12328: contig of 894 bp in length * 12329 13231: contig of 995 bp in length * 12329 13231: contig of 903 bp in length * 13232 14127: contig of 896 bp in length		949.5 10319; contig of 885 bp in length 20320 21222; contig of 985 bp in length 21223 22101; contig of 973 bp in length 21223 22101; contig of 879 bp in length 22102 23010; contig of 879 bp in length 23011 23881; contig of 879 bp in length 23011 23881; contig of 879 bp in length 23882 24775; contig of 879 bp in length 32882 24775; contig of 879 bp in length	# 24776 25667: contig of 892 bp in length # 25668 26533: contig of 866 bp in length # 2654 27420: contig of 866 bp in length # 2654 27420: contig of 87 bp in length # 27421 28313: contig of 893 bp in length # 28314 29205: contig of 893 bp in length # 29206 30104: contig of 892 bp in length # 30105 31004: contig of 899 bp in length # 30105 31008: contig of 904 bp in length # 31009 31897: contig of 899 bp in length # 31009 31897: contig of 899 bp in length # 31898 32805: contig of 899 bp in length # 31898 32805: contig of 899 bp in length	33697; cont.i. 34581; gap of 34581; cont.i. 35473; cont.i. 35473; cont.i. 37239; cont.i. 38129; cont.i. 39012; cont.i. 39012; cont.i. 4806; cont.i. 41670; cont.i. 42550; cont.i. 42550; cont.i. 42550; cont.i. 43411; cont.i.
ORGANISM Homo sapiens Electronia Metazos; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE (bases 1 to 97339) AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E. TILE Homo Sapiens, Clone RP11-7R18 FFFFRENCE (bases 1 to 07239)	BBIT GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TESTAYOR, S., TITTELL, A., VASSAILEY, H., VORA., Wheeler, J., Wu, X., Whealer, J., Wu, X., Muncarian, S., C., TITTEL DIRECT Submission JOURNAL Submission JOURNAL Submission JOURNAL SHORT STP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA COMMENT On Dec 7, 1999 this sequence version replaced 91:6001999. All repeats were identified using RepeatMasker. All repeats were identified using RepeatMasker. All repeats washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR	www-s www-subm it Infi infi infi is eque is that is eque that that is eque that is eque is occup.	# 873: contig of 873 bp in length # 874

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AC008013 168986 bp DNA PRI 09-OCT-1999
Homo sapiens 12p12-21.3-21.8 BAC RPCII1-551L14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
AC008013 GI:5801645
                                                                                                                                                   Nomita, N. and Oharao.

Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro

DNA Res. 5 (1), 31-39 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLAARROEGRATVRALMFNAFSLQAKVWÄTMLAFVLERRRKKARLÖMALQAYQGÖLLÖ
BGAATRLLERAAGMKASROOLQAOQOYQAAHSIJIRAYBRCATLIKKOKYLGRGKRPOPLA
ALAPSRKYTFEGPLLINTIAAGAGDGTLETKRPQASRPLGALGRLAAEEPHALEL"
1516 c 1601 g 1003 t
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                                                            Submitted (13-FEB-1998) to the DDBJ/EMBL/GenBank databases. Osamu Ohara, Kazusa DNA Research Institute, DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Faz:+81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 TGCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA 92
                                                                                                                           2 (sites)
Nagase,T., Ishikawa,K., Miyajima,N., Tanaka,A., Kotani,H.,
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Pred. No. 11;
0; Mismatches 27; Indels 0
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/sex="male"
Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 5280)
Obara, O., Nagase, T. and Ishikawa, K.
Direct Submission
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/db_xref="taxon:9606"
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394. .3300
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1. .5280
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/gene="KIAA0542"
394. .3300
/gene="KIAA0542"
                                                                                                                                                                                                                                                                                                                    /clone-"HG4325
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Best Local Similarity 63.5%;
Matches 47; Conservative (
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4840 ACTTTCAACTGCAG 4853
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KIAA0542 protein.
Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK ppus clone:HG4325.
Homo sapiens
Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 TCIGGGCIGCCCCTTGTCCTCCTCTTGACCCTCGCAGCTCACATGGAACAGGGCCG 85
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Homo sapiens mRNA for KIAA0542 protein, complete cds.
AB011114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 44; Length 97339;
Pred. No. 9.9;
0; Mismatches 21; Indels 0
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g of 886 bp in length
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gap of unknown length
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gap of unknown length
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standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at TRL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                      Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
Number of consensus changing edits:
Number of N's in consensus :
                                                                                                                                                                                                                                                                                                 values in estimate:
                                                                                                                                                               QUALSTAT-REPORT-
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4287
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102546
102547
109591
109596
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165391
165392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (02-SEP-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases I to 168986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submission Submission Submitted (09-C2T-1999) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 28, 1999 this sequence version replaced g1:5739545. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (10-JUL-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 168986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 168986)
                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168986)
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Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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KEYWORDS
SOURCE
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ctggricta())icccgctc cgcctcgca(g)icccgcctc atggggitc(g)aaagacctgg catgagcca(g)ccttgcctg gaccatcgt(g)aagcccagg

atgggggtcc(n)aagagcctgg catgagccca(n)ccttgcctgt gaccatcgtg(n)aagccccagg

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Original+Context
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ccgcctcgca(n) teccogoctc

Edited+Context

168986 165936 0.000156145 0.03878

--- Summary Statistics ---

gggtaaccc(c)acttggcctt ggtaacccc(a)cttggccttt tttgtttttg(t)tttgttttgt ttttgftttg(t)tttgtttttt tgcatgtgtg(0)gtgcatatgc

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aaggaaggaa (g)gagggaagga aggaaggaag (g)agggaaggaa aactcaaaaa (g)gggtgcagca

/note="Region: 0146h06.sl Homo sapiens cDNA, AA91707l"
complement(1338. 1761)
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/rpt_family="MIR"
complement(725. .1166)
/rpt_family="MER110A" /rpt_family-"MER112" 3343. 3431 Version: 1.01 xfgc. Location/Qualifiers 2 10001 9001 7001 5001 3001 2001 bases repeat_region repeat_region repeat_region repeat_region repeat_region misc_feature FEATURES

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the

ANNOTATION OF FEATURES:

Features listing

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage. DUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality

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Homo saptens

Eutheria; Primates; Catarrhini; Hominidae; Wertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 36425)

Bukaryota, Macans, C., Balley, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Bavdd, R., Deshazo, D., Ding, T., Chen, T., Cox, C., David, R., Deblado, O., Deshazo, D., Ding, T., Domah-Rashid, N., Dugan-Rocha, S., Duutbin, K. J., Fernandez, C., Ferragito, D., Procum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L., Gorrell, Cucharge, O., Liu, J., Enthage, J., Hodgson, A., Hoques, M., Mallars, C., Modg, K., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Luk, W., Lodgan, O., Lu, J., Lucier, R., Martin, R., Martiner, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S., Shah, B., S., Nelson, A., Muyen, R., M
Homo sapiens clone RP11-608E13, *** SEQUENCING IN PROGRESS ***, 175
unordered pleces.
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complement(0268...10682)
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complement(11446...1596)
/rpt_family="MIR"
11657...11702
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complement(11703...11892)
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'db_xref="dbsTs:65709"
.1893. .12228
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complement(5216. .5329)
/rpt_family="MIR"
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5915. 5937
/rpt_family="(TGGG)n"
6552. 6842
/rpt_family="Alusx"
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/rpt_family="AluJo"
17370. .17389
                                          /rpt_family="MIR"
3432. .3508
/rpt_family="(TTCC)n"
3509. .3688
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AC009533 179622 bp DNA HTG 19-NOV-1999
Homo sapiens clone RP11-22823, *** SEQUENCING IN PROGRESS ***, 26
unordered pieces.
AC009533 AC009533 6 G1:6143848
HTG; HTGS_PHASE1.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179622)
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contig of 1198 bp in length gap of unknown length contig of 1199 bp in length contig of 1199 bp in length gap of unknown length length gap of unknown length gap of unknown length contig of 1199 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 118 bp in length gap of unknown length contig of 113 bp in length gap of unknown length contig of 113 bp in length gap of unknown length contig of 112 bp in length gap of unknown length contig of 112 bp in length gap of unknown length contig of 111 bp in length gap of unknown length contig of 111 bp in length gap of unknown length contig of 111 bp in length
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contig of 1110 bp in length
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contig of 1101 bp in length
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Best Local Similarity 63.5%; Pred. No. 12;
Matches 47; Conservative 0; Mismatches
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   RESULT 12
AC009533/c
LOCUS
DEFINITION
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AUTHORS

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TGVFTDKDKAAAHLKGGAKKVVISAPSKDAPMFVGVYEHEYKSDLAIV9BASCTTU
LAPLAKVINDREGIVEGLMTVUSITATQKTVDGPSMKDWRGGRAASFNIIPSSTGAA
KAVGKVLDQLAKKLIGMSFRVPTVDVSVYDLTVALEKAATYDEIKKAIKESSQGKLKG
LIGYTEDDVVSTDFVGDNRSSIFDAKAGIALSDNFVKLVSWYDDEMGYSTRVDLIIH
MSKA."
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/db_xref="G1:1143"
/db_xref="Strot:p04796"
/db_xref="
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
Rosidae; Capparales; Brasslcaceae; Sinapis.

| (bases 1 to 1091)
Martin, M. and Cerff, R.
Prokaryotic features of a nucleus-encoded enzyme. CDNA sequences for chloroplast and cytosolic glyceraldehyde-3-phosphate dehydrogenases from mustard (Sinapis alba)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 54671 IGCCCCTCCGGAAGCTIGGAIGCCCTCCACACCCTCTIGATCTTCCCTGTGAIGTCAC 54612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30.8; DB 43; Length 179622;
Pred. No. 12;
0; Mismatches 27; Indels 0;
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dehydrogenase; glyceraldehyde-3-phosphate dehydrogenase.
white mustard.
174533: contig of 1026 bp in length 174553: gap of unknown length 175472: contig of 899 bp in length 175472: gap of unknown length 176316: contig of 844 bp in length 176359: gap of unknown length 177169: contig of 833 bp in length 177189: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                886 others
                                                                                                                                                                                                                                                                                       177997: contig of 808 bp in length 178017: gap of unknown length 178814: contig of 797 bp in length 178834: gap of unknown length 179622: contig of 788 bp in length.
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Location/Qualifiers
1. .1091
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/organism="Homo sapiens"
/db_ref="taxon:9606"
/clone="RP11-22B23"
50451 a 39939 c 39369 g 48977 t
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/db_xref="taxon:3728"
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Best Local Similarity 63.5%;
Matches 47; Conservative
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                           Bodder B., Bouch, J., Carter, M., Chacko, J., Chan, S., Bulay, C., Burket, C., Burket, J., Bulay, C., Burket, J., Bulay, C., Burket, C., Burket, J., Carter, M., Chacko, J., Chen, S., Cox.C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, L. L., Guevara, W., Harris, K., Hernandez, C., Ferraguto, D., Kaelly, S., Kondelswaki, N., Koon, L. E., Jackson, L., Jackson, L., Jackson, L., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucier, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Mayton, R., Stam, M., Sparks, A., Stangs, A., Stangs, R., Stand, R., Matliamson, R., Matlian, Matlian, Matlian, Matlian, Matlian, Matlian, R., Matlian, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA
On Oct 30, 1999 this sequence version replaced gi:6139077.
* NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pleces
* so not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
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of 1420
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of 1182
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COMMENT

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MMCARH 1098 bp mRNA RDD 11-MAR-1997
M.musculus mRNA for coxsacklevirus and adenovirus receptor (mCAR)
                                         Direct Submission
Submitted (03-JAN-1997) J.M. Bergelson, Dana-Farber Cancer
Institute, Division of Infectious Diseases, 44 Binney Street,
Boston, MA 02115, USA
Z. (bases 1 to 1098)
Bergelson, J.M. Cuningham, J.A., Droguett, G., Kurt-Jones, E.A.,
Krithivas, A., Hong, J.S., Horwitz, M.S., Crowell, R.L. and
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1098)
                    8 GCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCCTCCTTGACCCTTGGCAGC
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Isolation of a common receptor for Coxsackie B viruses and adenoviruses 2 and 5
adenoviruses 2 and 5
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                                                                                        68 TCACATGGAACAGGCCGGGTATGACTTTGCAACTG 103
                                                                                                              Location/Qualifiers
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Quelle, D. E., Ashmun, R.A., Hannon, G.J., Rehberger, P.A., Trono, D.,
Quelle, D. E., Ashmun, R.A., Hannon, G.J., Rehberger, P.A., Trono, D.,
Brichter, K.H., Walker, C., Beach, D., Sherr, C.J. and Serrano, M.
Direct Submission
Submission
Submitted (14-APR-1998) Immunology and Dncology, National Center of
Blotechnology, Campus de Cantoblanco, Madrid E-28049, Spain
1. 1301
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AMGRIPPDLAEDQGREDIARTLABATGD"

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Quelle, D.E. 1, Ashmun, R.A., Hannon, G.J., Rehberger, P.A., Trono, D., Richter, K.H., Walker, C., Beach, D., Sherr, C.J. and Serrano, M. Clohing and characterization of murine pl6INK4a and pl5INK4b genes 05380169
                                                                                                                                                                                                                                                                                                                                                                      ArUS9567 1301 bp mRNA ROD 22-APR-1998 Was musculus cyclin dependent kinase inhibitor 2B (Cdkn2b) mRNA, AF059567
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Local Similarity 63.9%; Pred. No. 13;
nes 46; Conservative 0; Mismatches
1075. .1080
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1091
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234 c 285 g
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

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March 20, 2000, 18:37:54; Search time 70.18 Seconds (without alignments) 641.701 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

Scoring table: IDENTITY_NUC

311585 seqs, 125096042 residues Searched:

N_Geneseq_36:* 0 Word size :

Database :

623170 Number of hits that pass the threshold : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	cription	Ruman stomach carc		Cell-cycle regulat	Mouse coxsackievir	EST clone AR34. Ne	Human brain-specif	Serine protease fo	ADP ribosylation f	Sequence encoding	Wnt-10b gene. Expr	New TGF-beta famil	Cartilage-derived	Human bone morphog	DNA encoding human	cDNA encoding huma	DNA encoding human	cDNA for human MP5	Human MP52 cDNA. M	Hepatitis C virus	cDNA encoding a mu	Prostate cancer as	FE65 cDNA. Peptide	Nucleotide sequenc	Secreted protein F	EST clone FB78. Ne	Gene No. 12 encodi	ij	EST clone AA299. N	-Delta-1 gene (1 gen	Chicken liver alph	alpha-	cen	BBC6 qene for requ	sequence u	DNA seguence used	clone FW	Degenerate lipocal	Parathyroid hormon
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		RESULT V84366 ID V	S I	E E	X C	3 E	F		Z	2 5	R K	PA	PA	200	ž Ľ	ቯ	PS	ខ្ល	ខ	ខ្ល	38	ខ	႘	មួម	ខ	ខ្ល	3 5	ខ	ပ္ပ ၀	1	OME	ò	윰	δλ	셤	δy	g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRA encoding coxsackie virus and adenovirus receptor - useful for modulation of e.g. cardiac, pancreatic or gastrointestinal infection by DRA encoding coxsackie virus and adenovirus and secure; Fig 14; 104pp; English.

The present sequence encodes mouse coxsackievirus and adenovirus consciours; Fig 14; 104pp; English.

The present sequence encodes mouse coxsackievirus and adenovirus considered represent invention also describes: (1) a method for modulates CAR protein activity or CAR nucleic acid expression, which modulates CAR protein activity or CAR nucleic acid expression, associated activity of the cell in the absence of the agent; and (2) a method for detecting the presence of CAR in a biological sample comprising contacting a biological sample with an agent capable of detecting CAR protein or mRNA such that the presence of CAR is detected.

COMPATISING contacting a biological sample with an agent capable of detecting CAR protein or mRNA such that the presence of CAR is detected.

COMPATISING contacting a biological sample with an agent capable of confluction of CAR is useful for treatment of cardiac infection, e.g. myocarditis, pericarditis or dilated cardiomyopathy, or infection of the central nervous system, e.g. a non-specific febrila lilinose or infection of the respiratory or gastrointestinal tract or childhood onset diabetes mellitus. Probes derived from CAR nucleic acids are useful for hybridisation assays, and antibodies raised against CAR include combining CAR protein and candidate/test compound are useful in sequence liles BP; 297 A; 1286 C; 288 G; 257 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                          03-AUG-1998 (first entry)
Mouse coxsacklevirus and adenovirus receptor encoding DNA.
Mouse, coxsacklevirus, adenovirus; receptor; CAR, cardiac infection;
myocarditis; pericarditis; dilated cardiomyopathy; meningoencephalitis;
panoreatic infection; acute pancreatitis; gastrointestinal tract;
diabetes mellitus; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCTCCTT 61
                                                                                                                                                                                                                                                                                                                             /*tag= a
/*tag= a
/*tag= a
/product= "coxsacklevirus and adenovirus receptor"
/product= "coxept= (pos:1096, .1098,aa:Xaa)
/rote= "Xaa= a stop codon, the sequence is shown as
continuing but gets unclear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.8%; Score 32; DB 1; Length 1128; 62.5%; Pred. No. 0.21; tive 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-1996; US-026100.
(DAND ) DANA FARBER CANCER INST INC.
Bergelson JM, Finberg RW, Horowitz MS;
WPI: 98-207384/18.
                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .1128
                                             V28846 standard; DNA; 1128 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               772 ITCIGCIGICACAGGAAAGG 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GCCAGCTCACATGGAACAGG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 62.55
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-1997; U16189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W57213.
                                                                                                                                                                                                                                                    Mus sp.
Key
CDS
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P-F50B; R851B.

The P-F50B; R851B.

The clated nucled calds, antibodies etc., used in diagnosts and related nucled calds.

Therapy of abnormal call proliferation, degeneration etc.

Claim 43: Page 81-82; 109pp; English.

Claim 43: Page 81-82; 109pp; En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GCGGTGGCCAGGCCCGCGTCACTGCTGCCCCAACATGCCCTTGTCCCCGGTCGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding human receptor for adenovirus C and coxsackievirus B - for preventing and treating viral infection and rendering cells susceptible to transformation by adenoviral vectors in gene therapy Claim 2; Page 68-70; 88pp; English.
This cobs molecule codes for mouse MCAR protein (see W69699) that serves as cellular receptor for adenoviruses of the serotypes 2 and 5 (subgroup C) and for the group B coxsackieviruses (CVB). It was obtained by screening a lambda phage expression cDNA ilbrary with antiserum containing antibodies specific for mouse CVB binding protein p46, and was used to identify human HCAR CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1998 (first entry) Mouse coxsacklevirus and Ad2 and Ad5 receptor (MCAR) cDNA. MCAR; coxsacklevirus receptor; CVB; adenovirus; Ad2 receptor; Ad5 receptor; mouse; infection; vaccine; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 16.9%; Score 30.4; DB 1; Length 580;
1. Similarity 57.3%; Pred. No. 0.56;
55; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                25-WAY-1994, US-248812.
14-SEP-1994; US-346511.
29-WOV-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
WPI; 95-373798/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 TCACATGGAACAGGGCCGGGTATGACTTTGCAACTG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 C;
Location/Qualifiers
91. 483
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157. .1215
/*tag= a
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V50430;
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30-ZAN-1999; U01724.
30-ZAN-1997; US-036986.
(UTNY ) UNIV NEW YORK STATE.
PALIDSOO L. TOMKO RP;
WPI: 98 437397/37.
P-PSDB; W69698.
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                                                                                  /*tag= a
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Best Local Similarity
Matches 55; Conserv
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26-OCT-1995.
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15-CCT-1998.

16-RAPE-1998.

10-APRE-1998.

10-APRE-1998.

10-APRE-1998.

10-APRE-1999.

10-APRE-1997.

10-APRE-197.

10-APRE-107.

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EST clone AR34.
Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                             868 ACGATCGCGGCGCCGTCATAGGCACGCTGCTGGCCCTTGTGCTCATCGGGGCCATCCTC 927
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                   2 AGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCTCCTT 61
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(see V50429). The invention also provides host cells transformed with DNA molecules encoding HGAR or MGAR and methods of producing the recombinant proteins or their derivatives. These proteins, their extracellular domains, as well as oligopeptides (see W69699-708) which bind virus, are also provided. Isolated HGAR or MGAR proteins or their fragments or variants are used to prevent or treat virus infections. Expressing the DNA in cells which lack these viral receptors renders the cells susceptible to transformation by adenoviral vectors carrying genes for gene
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                                                                                                                                                                                                                                                                                      Ouery Match 16.9%; Score 30.4; DB 1; Length 1301; Best Local Similarity 61.2%; Pred. No. 0.76; Matches 49; Conservative 0; Mismatches 31; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.6%; Score 29.8; DB 1; Length 291; 70.2%; Pred. No. 0.69;
                                                                                                                                                                                                                            297 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 T;
                                                                                                                                                                                                                            322 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                            327 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
V86365CID V86365 Standard; CDNA; 291 BP.
AC V86365;
AC V86365;
                                                                                                                                                                                                                            355 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       928 TICIGCIGICACAGGAAACG 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GGCAGCTCACATGGAACAGG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                            1301 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                          therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Human and rat-derived brain-specific adaptor polypeptide FC99 - is involved in neuron signal transmission and is useful in diagnosis and rat-derived brain-specific adaptor in diagnosis and treatment of neurological diseases e.g. Alzheimer's dementia and treatment of neurological diseases e.g. Alzheimer's dementia and reatment of neurological diseases e.g. Alzheimer's dementia and claim 4; Pages 22-23; 42pp; Engilsh.

A cDNA clone (766986) codes for FC99 (W15256), a novel brain-specific adapter molecule involved in neuron signalling pathways.

It was obtd. from a normalised cDNA library prepd. from human cerebrum-derived mRNA. 5'-Terminal sequences of plasmid inserts in E. coll transformants were sequenced and translated amino acid corebrain cortex), was selected. Sequencing revealed RC99 (FC - forebrain cortex), was selected. Sequencing revealed alternative, in-frame initiation points of translation, providing coding sequences of 1425 bases (T66883) and 1785 bases (T66886). FC99 culcied acids (including antisense) and polypeptides can be used to study phosphorylated tyrosine-mediated intracellular signalling pathways in diagnosis and treatment of neurological diseases and cortext diagnosis/treatment methods or reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 CCACTATGGGGTCTGGGCTGCCCTTGTCCTCTTGACCCTCCTTGGCAGCTCACATG 74
                                                                        Human brain-specific adapter FC99 cDNA.

Brain-specific adapter; FC99, neuron; signal transmission;
neurological disease; Alzheimer's disease; Parkinson's disease;
diagnosis; therapy; tyrosine kinase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.0%; Score 28.8; DB 1; Length 1785; 62.5%; Pred. No. 2.9; tive 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-1995 (first entry)
Serine protease for fusion protein cleavage.
Serine protease, Factor-Xa; recognition site,
fusion protein cleavage; protein folding; ds.
T66986 standard; cDNA to mRNA; 1785 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
76. 1554
/*tag= a
76. 1551
/*tag= b
                                                                                                                                                                                                                                               14-MAY-1997.

11-CCT-1996; 116333.

13-OCT-1995; JP-26598.

12-DEC-1995; JP-323069.

29-FEB-1996; JP-069265.

4-UUL-1996; JP-069265.

(SUME ) SUMITOMO ELECTRIC IND CO.

Nakamura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q71243 standard; cDNA; 1554 BP. Q71243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.59
Matches 45; Conservative
                              T66986;
30-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 GCCGGGCGCGG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 GAACAGGGCCGG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 97-261318/24.
P-PSDB; W15256.
                                                                                                                                                                                                 Homo sapiens.
EP-773291-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9418227-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
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64 GCCAGCAGGCGCCTGGGCAGCCCCTGGGCCCCTCTGGCCCCATCTTCGG 15
                                                                                                                                                                                                                                                                29-DEC-1989; 313687
29-DEC-1988; US-291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                              WPI; 90-203091/27.
P-PSDB; R05711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal_peptide
                                                                                                                                                                                                                                   EP-376746-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wnt-10b gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9640910-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
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T49318
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7. ASPR-1995; 105287.
8. SAPR-1994; JP-071048.
8. SAPR-1994; JP-071048.
8. SAPR-1995 BERWERIES.
11 Hirota N. Ito K, Kuroda H;
12 MPI; 95-375210/49.
12 MPI; 95-375210/49.
13 Page 7-9; J4pp: Bagglish.
14 From an ADP Tibosylation factor gene of a plant
15 Claim 3; Page 7-9; J4pp: Bagglish.
16 Abarley ADP Tibosylation factor (ARF) gene was isolated by differential screening of cDNA libraries prepd. from barley roots and leaves. The regulatory (promoter) region of the gene was identified and sequenced (T05628). This region has been incorporated into and sequenced (T05628). This region has been incorporated into express genes in a tissue-specific, efficient manner for use in plant breeding or the prodn. of substances using plant tissues or cells.
15 Sequence 3088 BP; 716 Å; 761 C; 672 G; 939 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                71 CCACCATGGGGGCCTGCTGCTTCTTGCTCACACGCCCTTGGGGGGCCCTCCTGC 130
                                                                                                                                                                                                                                                                                                                                                                                                                 75 GAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAGTTCCT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                            131 GGCCGGCGGGAGCGTGTTCTGCCCCGGGACCAGGCCCACCGTGTCTGCAGAGAGCCC 190
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                     15 CCACTATGGGGTCTGGCCTGCCCTTGTCCTCTTGACCCTCCTTGGCAGCTCACATG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                          refolding of polypeptide molecules - using a cyclic process involving denaturing and renaturing conditions to produce a correctly folded prod

10 bischosure: Page 112-114; 202pp; English.

New recombinant serine protease shows narrow substrate specificity for the Factor-Xa cleavage site, and may replace Factor-Xa for cleavage of fusion proteeins engineered to include this site.

Sequence 1554 BP; 315 A; 488 C; 528 G; 223 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds.
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105628 standard; DNA; 3088 BP.
105628;
15-FEB-1996 (first entry)
ADP ribosylation factor gene regulatory region.
ADP ribosylation factor; promoter; ARF gene; vector; barley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.3%; Score 27.6; DB 1; Length 3088; Best Local Similarity 72.0%; Pred. No. 8.8; Matches 36; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                     Query Match 15.9%; Score 28.6; DB 1; Length 1 Best Local Similarity 49.0%; Pred. No. 3.2; Matches 76; Conservative 0; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 GCCACIAIGGGGTCTGGGCTGCCCCTTGTCCTCTGACCCTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/function= ADP gene promoter region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 GCAGGGCCAACTCATTCTTGGAGGAGGTGAAGCAG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 CCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAG 169
                                                                                  Thogersen HC;
04-FEB-1994; DK0054.
04-FEB-1993; DK-000130.
05-FEB-1993; DK-000139.
03-DEC-1993; WG-G02492.
(DENZ-) DENZYME APS.
                                                                             Etzerodt M, Holtet TL, WPI; 94-279681/34.
P-PSDB; R60502.
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1144 GTCATCGTGGTCGTGGTGGTCGTCGTCGTCGTCGCGCATGGCCGTCCTGGTGATCACCAAC 1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GCCACTATGGGGTCTGGGCTGCCCTTGTCCTCTTGACCCTCCTTGGCAGCTCACAT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.2%; Score 27.4; DB 1; Length 2259; llarity 54.5%; Pred. No. 9.1; Conservative 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, Wht-10b; fetal bone marrow stroma cell; growth factor; antibogy; antisense; hematopoletic stem cell cultulre; gene therapy; ex vivo; diagnostic; ss.

Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor-associated antigen, GA733-2 -
Expressed in pacreatic carcinoma cells, used for tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. 193
| 1. 193
| 1. 193
| 1. 193
| 194. 1363
| 194. 256
| 194. 256
| 1857 | 1360
| 1858 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 1958 | 195
                                                                                                                                                                                Sequence encoding tumour associated antigen GA733-1. Pancreatic carcinoma; GA733-1; cancer; ds. Bomo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 GGAACAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGA 114
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
307. .1275
/*tag- a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T49318 standard; cDNA; 2122 BP.
Q05106 standard; DNA; 2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-1996.
06-UUN-1996; E02455.
07-UUN-1995; US-485449.
(SANO ) SANDOZ LTD.
(SANO ) SANDOZ PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1997 (first entry)
                                                                                                              02-NOV-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WIST-) Wistar Inst.
Linnenbach A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A PER PET TEST TO BE PET TEST TO BE
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78 25-MAY-1994; DE-420122.
79 1917-1994; DE-420127.
70 1917-1994; DE-420127.
70 1917-1994; DE-420127.
71 1917-1994; DE-420127.
72 1917-1994; DE-420127.
73 1917-1994; DE-420127.
73 1917-1994; DE-420127.
73 1917-1994; DE-420127.
74 1917-1994; DE-420127.
75 1917-1994; DE-420127.
76 1917-1994; DE-420127.
77 1917-1994; DE-420127.
78 1917-1994; DE-420127.
79 1917-1994; DE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                             Claim 3; Page 28-30; 46pp; English.

The sequence encodes human growth factor Wnt-10b, and has been isolated from a fetal bone marrow stroma cell CDNA library by PCR isolated from a fetal bone marrow stroma cell CDNA library by PCR isolated from a fetal bone marrow stroma cell cDNA library by PCR isolated for sequences within the Wnt gene family, followed by use of the amplified fragment as a probe and chromosome walking for isolation of the full-length sequence. A truncated sequence, Wnt-10b-delta, is given in 149319 (Claim 3). A plasmid containing the Wnt-10b cDNA has been deposited as Arcc 97208. Antibodies and antisense sequences corresponding to Wnt-10b may be used as pharmaceuticals, and Wnt-10b may be used in a culture medium for ex vivo haematopoietic stem cell culture for use e.g. in gene therapy. Fragments of the gene may be used as claquostic probes or primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-1995 (first entry)
New TGF-beta family member - MP-52 DNA sequence.
Transforming growth factor-beta family; mitogenic; differentiation;
treatment; prevention; disease; bone; cartilage; connective tissue;
skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
tissue regeneration; arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 GAACAGGCCGGGTATGACTTTGCAACTGAAGGAGGTCTTTTCTGACAAGTTCCT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             715 CCACTCTCTGCCCAGCCCTGGCCTCAAGCCCCAGGCCCTGGCCCCCAGGACACATG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 CCACTATGGGGTCTGGGCTGCCCCTTGTCCTCTTGACCCTCCTTGGCAGCTCACATG 74
                                                                                                                     sequences - used for selection, expression and isolation of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.1%; Score 27.2; DB 1; Length 2122; 51.7%; Pred. No. 10;
                                                                                                       Expression vectors and methods for cloning N-terminal signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= MP-52 TGF-beta propeptide 1783. .2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
(SANO ) SANDOZ-ERFINDUNGEN VERW GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
640. .2145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start- 1783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               083695 standard; DNA; 2703 BP. Q83695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 51.79
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE-326829.
                (SYST-) SYSTEMIX INC.
Van Den Berg DJ;
WPI; 97-052317/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E02630.
                                                              WPI; 97-052317,
P-PSDB; W08928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FEB-1995.
09-AUG-1994; E
10-AUG-1993; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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has mitogenic and/or differentiation inducing properties useful in the treatment or prevention of diseases of bone, cartilage, connective tissue, skin, mucosa, epithelium or dental tissue. The protein can also be used for wound healing and tissue regeneration e.g. in osteoporosis and arthritis.
                                                                                                                                                                                                                                                                                                                                  2449 GCCCACCATTCTCCTCACCTGGGCCTTCTCACCTCTGGACTCTCCTAAGCACTCTCA 2508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New purified cartilage extracts and proteins - used to stimulate the development and repair of cartilage in vivo.

Claim 10; Fig 1: 34pp: English.

Claim 10; Fig 1: 34pp: English.

The sequence encodes human articular cartilage-derived morphogenetic protein-1 (CDMP-1). Primers T13603-06, constructed from conserved motifis from bone morphogenetic protein, have been used in reverse transcription-polymerase chain reaction amplification of a cattle articular chondrocyte cDNA library, generating products of 120 and 280 bp, which are then used to screen a human articular cartilage CDNA library. Colne lacking the N-terminal region has been isolated, and used to obtain a full-length genomic clone.

CDMP-1 is present in a purified cartilage extract (claimed) which
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                    13 GGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCTTGACCCTCCTTGGCAGCTCACA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/roduct= Cartilage-derived morphogenetic protein-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product Mature C-terminal domain
1501. 1620
/*tag= g
//tote= "PCR-amplified probe used to screen cDNA
1brary"
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                                                                                                                                                                                                        DB 1; Length 2703;
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Cartilage-derived morphogenetic protein-1 gene.
Human; cartilage-derived morphogenetic protein-1; CDMP-1;
articular cartilage; chondrogenic; vulnerary; implantation,
chondromalacia; osteoarthritis; therapy; joint repair; ss.
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                  Score 26.8; DB 1; I
Pred. No. 15;
0; Mismatches 22;
                                                                                                                         784 G;
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265. .1770
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322. 1767
/*tag- d
/product- Pro-CDMP-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-1996.
07-MOV-1994; U12814.
07-NOV-1994; WO-U12814.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Chang SC, Luyten FP, MOOS M;
                                                                                                                         758 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= e
/note= "cDNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cocation/Qualifiers
1. .381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lori HEALTB & BUMAN Chang SC, Luyten FP, Moos M; WPI; 96-251714/25.
                                                                                                                         602 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T31601 standard; DNA; 2341 BP
                                                                                                                                                                                                14.9%;
milarity 64.5%;
Conservative 0
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Best Local Similarity
Matches 40; Conserva
                                                                                                                         2703 BP;
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25-0CT-1996
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T31601
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2449 GCCCACCATTCTCCTCACCTGGGCCTTCTCAGCCTCTGGACTCTCCTAAGCACCTCTCA 2508
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                                                                                                                                                                   13 GGCCACTATGGGGTCTGGGCTGCCCTTGTCCTCTTGACCCTCCTTGGCAGCTCACA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human bone morphogenic factor, MP52 Arg - used in the treatment of osteoporosis and bone fracture, and for promoting bone regrowth claim 1. Page 12-15; 26pp; English engine of promoting bone regrowth a cDNA fragment in plasmid pMSS99 (T59729) codes for novel human bone morphogenic factor MP52 Arg (W12770), a growth factor that induces formatings from undifferentiated mesenchymal cells and which stimulates the differentiation and maturation of osteoblasts. Plasmid pSK52s was digested with Hindill, and the isolated DNA fragment (config. cDNA comprising the compilete region for MP52 Arg) was inserted into vector pABStop to give pMSS99. This expression vector can be used to produce MP52 Arg in host
stimulates local cartilage formation and repair when combined with a matrix and implanted in a mammal. The protein may be used in therapy of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or to repair cartilage after reconstructive surgery. Sequence 2341 BP; 523 A; 688 C; 683 G; 447 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (e.g. CHO) cells for use in the treatment of osteoporosis and bone fracture, and for orthopedic reconstruction, bone transplantation. cosmetic surgery and dental implantation. 784 G; 559 T;
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                                                                                                         DB 1; Length 2341;
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                                                                                                                                                                                                                                                                                                                                                             11-MAY-1997 (first entry)
Human bone morphogenic factor MP52 Arg; bone; cartilage; skin;
Bone morphogenic factor; MP52 Arg; bone; cartilage; skin;
connective tissue; mucous membrane; epithalium; teeth;
wound healing; vulnerary; tissue regeneration; osteoporosis;
bone fracture; dental implant; osteoblast; pMSS99; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.9%; Score 26.8; DB 1; Length 270;
64.5%; Pred. No. 15;
iive 0; Mismatches 22; Indels
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(BLOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.
Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576. .2279
/*tag= d
/note= "bases 576-2279 comprise the MP52
                                                                                                                                     22; Indels
                                                                                                       Query Match
14.9%; Score 26.8; D
Best Local Similarity 64.5%; Pred. No. 15;
Matches 40; Conservative 0; Mismatches
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/40. .2145

/4189- a

640. 720

/*189- b

/*189- c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence in pMSS99"
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Best Local Similarity 64.59
Matches 40; Conservative
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02-AUG-1996; E03427.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujino Y, Kawa.
WPI, 97-154261/
P-PSDB; W12770.
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T59729
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13 GGCCACTATGGGGTCTGGGCTGCCCTTGTCCTCTTGACCCTCCTTGGCAGCTCACA 72

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28-CCT-1997 (first entry)
CDNA encoding human protein MP52, a growth/differentiation factor.
Growth factor, diferentiation; bone induction; osteoporosis; teeth;
tooth; dental; joint lissue; cartilage; mucous membrane; skin; nails;
wound healing; regeneration; skeletal disorder; fracture; dimer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes the human MP52 protein, which is described in W0 9316099 and 9504819 as a member of the human transforming growth factor beta superfamily. Active MP52 can be used in a medicament to treat and prevent nervous system diseases, and/or to treat neuropathological conditions caused by nervous system againg.

602 A; 758 C; 784 G; 559 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicaments contg. protein MP52 - useful for treating neurological
                                                                                                                                                                                                                                                         15-OCT-1997 (first entry)

DNA encoding human MP52 protein.

Human; MP52; transforming growth factor; TGF; beta; medicament; treatment; prevention; nervous system; disease; neuropathology; ageing; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bechtold R, Hoetten G, Paulista M, Pohl J, Unsicker K; WPI; 97-078343/08.
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0; Mismatches
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T61412;
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640. .2145
/*tag= a
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640. .2145
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24-JUL-1995; JP-218022.
(FARH ) HOECHST JAPAN LID.
(FARH ) HOECHST PHARM & CHEM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product- MP52
                                                                                                                                                                                                              T59405 standard; DNA; 2703 BP. T59405;
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12-JUL-1995; 025416.
12-JUL-1995; DE-025416.
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ses 40; Conserv
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2509 GG 2510
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Best Local Si
Matches 40;
                                                                                                                              RESULT 14
T59405
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Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;

WPI: 97-132636/12.

DR P5DB: T61412.

High molecular weight human MP52 growth or differentiation factor -

Promotes bone induction, is useful for treatment and prevention of

promotes bone induction, is useful for treatment and prevention of

Promotes bone induction, is useful for treatment and prevention of

Claim 1: Page 12-16; 25pp; Japanese.

Claim 1: Page 12-16; 25pp; Japanese.

Claim 1: Page 12-16; 25pp; Japanese.

Tolaim 2: Page 12-16; 25pp; Japanese.

Tolaim 2: Page 12-16; 25pp; Japanese.

Tolaim 3: Page 12-16; 25pp; Japanese.

Tolaim 1: Page 12-16; 25pp; Japanese.

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Query Match 14.9%; Score 26.8; DB 1; Length 2703; Best Local Similarity 64.5%; Pred. No. 15; Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps

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73 TG 74

2509 GG 2510 g

Search completed: March 20, 2000, 18:37:58 Job time: 8532 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

March 22, 2000, 01:22:33; search time 50.59 Seconds (without alignments) 425.974 Million cell updates/sec Run on:

US-09-092-296-3 180 1 CAGGACCGCAGTGGCCACTA......CITGAAAAGCTCTGCCTCT 180 Title: Perfect score: Sequence:

Scoring table: IDENTITY_NUC

214294 seqs, 59861208 residues Searched:

Issued_Patents_NA:*

0 Word size :

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Appli	App 11	Appli	App11	App11	85254	Appli	App11	App11	App11	Appl	Appl	App11	App11	Appli	App11	App11	App11	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1
		ø		,	i	1,	i	2	i	ä	ä	H	32,	32,	H	-1	H	m	4,	7	13	20,	21,	52	33	24,	22	, 26	27,	28,	3	30,	31,	32,
		Description	Sequence	Sequence	Sequence	Seguence	Sequence	Patent No.	Sequence	Sequence	Sednence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Sednence	Sednence
		ជ	US-08-627-610-7	PCT-US95-04636-7	US-08-469-486-1	US-08-469-658-1	US-08-418-444A-1	5185254-3	US-08-485-449-1	US-08-288-508C-1	US-08-937-466-1	US-09-172-528-1	US-08-222-616-32	PCT-US95-04228-32	US-08-406-070-1	US-08-665-617-1	US-08-689-190-1	90	US-08-689-190-4	œ	US-08-733-446-19	US-08-733-446-20	33-446	33-446	US-08-733-446-23	33-446	US-08-733-446-25		-08-733-446	-08-733-446-2	-08-733-446	-08-7	-08-733	US-08-733-446-32
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		Match Length	580	280	1554	1554	3088	2259	2122	2703	2782	2782	4425	4425	2334	944	252	263	265	655	234	237	240	243	252	245	247	248	250	251	253	254	256	263
æ	Query	Match	16.9	16.9	15.9	15.9	15.3	15.2	15.1	14.9	14.8	14.8	14.7	14.7	14.3	14.2	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1
		Score	30.4	30.4	28.6	28.6	27.6	27.4	•	•	•	26.6	26.4	26.4	25.8	25.6	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4	25.4
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7333 7333 7417 7417 750 760 760 760 760 760	ALIGNMENTS 0 Dos 7,610	re 30.4; id. No. 0.1 Mismatches ccccTTGTCC
008	LD C. An C.	Score 30.4; Direction of the process
US-08-733-446-36 US-08-733-446-56 US-08-733-446-57 US-08-733-446-61 US-08-733-446-61 US-08-733-446-62 US-08-758-746-62 US-08-758-746-62 US-08-758-76-858A-1 US-08-294-871A-1 US-08-294-871A-3 US-08-294-871A-3	ALIGNAME ALIGNAME A. Animal ton TELD TELD 7/627,610 CSI-001CP6 NN:	So Pro
®®®®®®®≠+0000	Aution US/08627610 NY: Ch, David H. Tano, Manuel Inho, Roanid A. CON: Transgenic P. MILVE & COCKFIELD ARTHVE P. TICON DAYA: FIOPPY disk FIOPPY disk FIOPPY disk TICON DAYA: TICON DAYA: TOON BOOTH TOON DAYA:	**************************************
	us/086. avid H. Manuel Manuel Manuel Transg Regula Regula Regula Regula SS: 6 COCK Street Dara Dara US/0 PR-1996 00 PR-1996 1 US/0 PR-1996 1 US/0 TICS: 7 TICS: 4 A	16.9%; 57.3%; ive idencir 111
265 252 252 252 234 252 1785 1785 1785 1785	ication US/ 1077	larity 57. Conservative
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	111cati 1997 199	arti Onse
	17-610-7/c nce 7, Application t No. 5919997 RLL INFORMITOR: PLICANT: Beach, De PLICANT: Serrano, PLICANT: Serrano, TLE OF INVENTION: TRESPONDENCE ADDRES RRESPONDENCE ADDRES RRESPONDENCE ADDRES RRENT BOSTON REDION TYPE: FLOPE COMPUTER: NAA REDION TYPE: FLOPE COMPUTER: BADABLE FOR MEDION TYPE: FLOPE COMPUTER: BADABLE FOR MEDION TYPE: TROPE FILLING DATE: 04-AR TELEPAN: 6(17) 22; TELECANT INFORME TELEPAN: 6(17) 22; TELEPAN: 6(17) 23; TELEPAN: 6(17) 23; TELEPAN: 6(17) 23; TELEPAN: 6(17) 22; TELEPAN: 6(17) 23; TELEPAN	th 1 Similarity 55; Conserv CAGTGGCCACTAI
44444444	1 127-610-7/c nce 7, Appl. RAL INFORMAND PLICANT: B6 PLICANT: B7 P	8319 55; 1111
223255555555555555555555555555555555555	1 10-77-610-7, Almore 7, Almore 8, Almore 8, Almore 8, Almore 8, Almore 8, Almore 8, Almore 9, A	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	ABESULT 1 US-08-627-610-7/C Sequence 7, Application US/08627610 Patent No. 5319979 GENERAL INFORMATION: APPLICANT: Bearch, David H. APPLICANT: Depthio, Ronald A. TITLE OF INVENTION: Regulation NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: ADDRESSES: LAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston STARE: MA COUNTR: USA ZIP: 03109 COMPUTE: IBM PC compatible COUNTR: USA ZIP: 03109 COUNTR: USA COUNTR: WA COUNTR: OS-SEATHORY OFBEATING SYSTEM: PC-DOS/MS-D SOFTWARE: ASCII(text) CORRAINO NUMBER: 36,709 REGISTRATION: NUMBER: GSI-794 INFORMATION FOR SEQ ID NO: 7: FELEPHONE: (617) 227-7440 TELEPHONE: (617) 227-7441 INFORMATION FOR SEQ ID NO: 7: ELENGTH: 580 Dase pairs TYPE: NUCLEC CHARACTERISTICS: LENGTH: 580 Dase pairs TYPE: CONCLOST: Linear MOLECULE TYPE: CDNA FEATURE: NAME/KEY: CDS US-08-627-610-7	Query Match Best Local S Matches 55 Watches 626 V 8 GCAG
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225 Franklin Street
                                                                  Massachusetts
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ORGANISM: Bos taurus
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76..1551
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MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
; LOCATION:
US-08-469-486-1
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                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses TITLE OF INVENTION: Related Thereto NUMBER OF SECURSES: 10 COMPUTER READABLE FORM: MEDIOW TYPE: Floppy disk COMPUTER: IRM PC COMPUTER: PROPEY disk COMPUTER: PIN PC COMPUTER: PROPEY ALSH PC COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08469486
; Sequence 1, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
APPLICANT: Thoegersen, Hans Christian
APPLICANT: Holtet, Thor Las
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
UNMBER OF SEQUENCES: 58
CORRESPONDEME ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.9%; Score 30.4; DB 6; Length 580; Best Local Similarity 57.3%; Pred. No. 0.12; Matches 55; Conservative 0; Mismatches 41; Indels
68 TCACATGGAACAGGGCCGGGTATGACTTTGCAACTG 103
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                                     68 AGAAATGGTCCTTCGCCGGCCGTGAGATTGCTACAG 33
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04636
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04636
FILING DATE: 29-NOV-1994
FILING DATE: 29-NOV-1994
FILING DATE: 29-NOV-1994
FILING DATE: 14-SEP-1994
FILING DATE: 14-SEP-1994
FILING DATE: 25-MAY-1994
FILING DATE: 25-MAY-1994
FILING DATE: 14-APR-1994
                                                                                                                                                                                                      Sequence 7, Application PC/TUS9504636
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: 91..480
PCT-US95-04636-7
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MOLECULE TYPE: CDNA
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75 GAACAGGGCCGGGTATGACTTTGCAACTGAAGGAGTCTTTTTTGACAAGTTCCT 134
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Patent No. 5917018
GENERAL INFORMATION:
FAPLICANT: Th egersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
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COUNTRY: USA
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.25
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CLASSIFICATION: 530
PROR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: FEBLUATY 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: PAUL T. CLARK
REGISTRATION NUMBER: 30, 162
REFERRINCE/DOCKET NUMBER: 30, 162
REFERRINCE/DOCKET NUMBER: 30, 163
REFERRINCE/DOCKET NUMBER: 00, 163
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAK: 200154
INPORMATION FOR EGO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
ILENGTH: 1554 base pairs
TYPE: NULLEA: acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
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ADDRESSEE: Fish & Richardson P.C.
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1144 gtcatcgtggtggtcgtggtggccctcgtcgccggcatggccgtcctggtgatcaccaac 1203
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                                                                                                                                                                                                                                                                                                  COMFUTER: TELEPPY disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/W-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,444A
FILING DATE: 07-APR-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: JP HEI 6-71048
FILING DATE: 08 APR-1994
ATTOMEY AAGHT INFORMATION:
NAME: Oblon, No. 577368man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 259-024-0
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 GGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-08-418-444A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3088 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 2259
5185254-3
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US-08-418-44A-1/C
US-08-418-44A-1/C
Sequence 1, Application US/0841844A
Patent No. 5773688
GENERAL INFORMATION:
APPLICANT: KNRODA, HISAO
APPLICANT: HIROTA, NAOHIKO
APPLICANT: TTO, KAZUTOSHI
TITLE OF INVENTION: GENE EXPRESSION VECTOR USING THE GENE
TITLE OF INVENTION: FACTOR
TITLE OF INVENTION: FACTOR
TITLE OF INVENTION: FACTOR
NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.9%; Score 28.6; DB 4; Length 1554; Best Local Similarity 49.0%; Pred. No. 0.77; Matches 76; Conservative 0; Mismatches 79; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 79; Indels
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION: B30
PRIOR APPLICATION: B30
PRIOR APPLICATION: B30
APPLICATION: UNBER: 06/192,060
FILING DATE: FEBRUATY 4, 1994
CLASSIFICATION: 300
APPLICATION: 300
APPLICATION: B42
CLESSIFICATION: G10
TELEPHONE: 617 642 5070
TELEPHONE: 617 642 5070
TELEFROME 617 642 5070
TELEFROME: 617 642 5070
TELEFROME: 617 642 5070
TELEFROME: 617 642 5070
TELEFROME: G17 642 5070
TELEFROME: TABLESTRICES: LENGTH: TYPE: ILENGTH: TYPE: ILENGTH: TYPE: TABLESTRICES: GOULD
TYPE: NOTITIONER: COULD
TYPE: NOTITIONER: CHARACTERISTICS: TYPE: ILENGTH: TABLESTRICES: GOULD
TYPE: NOTITIONER: CHARACTERISTICS: TYPE: ILENGTH: TABLESTRICES: GOULD
TYPE: NOTITIONER: CHARACTERISTICS: TYPE: NOTITIONER: CHARACTERISTICS: TYPE: ILENGTH: TYPE: NOTITIONER: TYPE: NOTITIONER: CHARACTERISTICS: TYPE: TYPE:
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225 Franklin Street
                                 CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 76..1551
US-08-469-658-1
                                                                                                             X: USA
02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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Sequence 1, Application US/08485449
Patent No. 5824789
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLECTIDE
TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 GAACAGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAGTTCCT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 CCACTAIGGGGTCTGGGCTGCCCTTGTCCTCCTTGACCCTTGGCAGCTCACATG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08288508C

Patent No. 5994094

GENERAL INFORMATION:
GENERAL INFORMATION:
HIGH APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
ITLE OF INVENTION: THE TGF- FAMILY
NUMBER OF EXQUENCES: 40

CORRESPONDENCE ADDRESS:
ADDRESSEE: Mikaldo, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.1%; Score 27.2; DB 2; Length 2122; Best Local Similarity 51.7%; Pred. No. 2.7; Matches 62; Conservative 0; Mismatches 58; Indels 0
                                                                                                                                                                                                                                                                                                                                             COUNTER 10.5A

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIOW TYPE: FIOPPY disk
COMPUTER: 12 PP COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,449
FILING DATE:
CLASSIFICATION: 536
ATTORNET/AGENT INFORMATION:
NAME: KONSKI, ANYOINETE F.
REGISTRATION INFORMATION:
TELECOMMUICATION INFORMATION:
TELECOMMUICATION INFORMATION:
TELECOMMUICATION INFORMATION:
TELECOMMUICATION INFORMATION:
TELEFAX: (415) 813-560
TELEFAX: (415) 813-560
TELEFAX: (415) 813-560
TELEFAX: (415) 813-560
TELEFAX: (212) 826 PATES
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2122 base pairs
TYPE: nucleic acid
STRANDEDNESS: SIAGLE
FFAMIREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 194..1360
US-08-485-449-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-288-508C-1
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2101 GAAAACCTCCGAGAGAAGGCAGAAGAGCAGCTGTTCTCGTTCTTGCCCTAAGGTGGAG 2042
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                                                                                                                                                                                                      DB 4; Length 2782;
                                                                                                                                                                                                   Query Match
14.8%; Score 26.6; DB 4; Length 2:
Best Local Similarity 53.3%; Pred. No. 5;
Matches 56; Conservative 0; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 2041 ATTCTGAGTCCTGCTGCTTGAACTGATGGAGGGAGTGCCCC 1997
                                                                                                                                                                                                                                                                                                                                                                                                         135 CCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk computed to compatible computed to compatible computed to compatible coperating System: PC-DoS/MS-DoS SOCTWARE: Patin (Genentech)

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/22,616

FILING DATE: 2-APR-1994

CLASSIFICATION DATA:

APPLICATION NUMBER: PCT/US93/00586

FILING DATE: 22-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CT/US93/00586

FILING DATE: 22-JAN-1993

RIDING DATE: 22-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Lec, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/08222616 Patent No. 5635177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/22-1994
TELEFAX: 415/922-9891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bennett, Erian D.
APPLICANT: Gooddel, David
APPLICANT: Lee, James M.
APPLICANT: Lee, James M.
APPLICANT: Rathews, William
APPLICANT: Tsai, Siao Blig
APPLICANT: Rood, William I.
: LENGTH: 2782 base pairs
; TYPE: nucleic acid
; STRANDENESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-172-528-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , TOPOLOGY: linear
US-08-222-616-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-222-616-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 GAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAGTTCCT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.8%; Score 26.6; DB 3; Length 2782; Best Local Similarity 53.3%; Pred. No. 5; Matches 56; Conservative 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-09-172-528-1/C
Sequence 1, Application US/09172528
SEQUENCE 2, Admaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENIES DRIVE
CITY: HILLSBORNOGH
STREET: 75 DENIES DRIVE
CITY: HILLSBORNOGH
STREET: 05 DENIES DRIVE
COUNTRY: USA
COUNTRY: USA
STREET: 94010
COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
OOPERATING STSTEM: PG-DOSS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/172,528
FILING DATE:
CLASSTFTAMMS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 CCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCC 179
        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/937,466
                                                                                                   CLASSIPICATION: 435
ATTORNEY/AGRY INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/COCKET WUNBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEFRAX: (650) 343-434.
TELEFRAX: (650) 343-434.
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 2782 Dass pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPRA: (650) 343-4341
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/937,466
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: Tinear
; MOLECULE TYPE: CDNA
US-08-937-466-1
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Best Loca Matches

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Sequence 1, Application US/08406070

Patent No. 5610063

GENERAL INFORMATION:
APPLICANT: Smith, Daniel S.
TITLE OF INVENTION: A DNA FOR TITLE OF INVENTION: A DNA FOR CORRESPONDENCES. 6
CORRESPONDENCE ADDRESSEE: Relaing, Ethington, Barnard, Perry 6 Milton
STREET: P.O. BOX 4390
3163 GACAGCCTTTCGCTGCACCTCTAGACACTGAAACCGGAACGGGCCCTGTAGATGTTT 3222
                                                                       101 CTGAAGCTGAAGGAGTCTTTTCTGACAAGTTCCTCCTATGAGTCCAGCTTCCTGGAATTG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0X-03-66-617-1/c
; Sequence 1, Application US/08665617
; Sequence 1, Application US/08665617
; GENERAL INFORMATION:
; APPLICANT: Xudong, Ylu
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1081 TGATCTTCCCACTGTACACGTCTTGCACCTCATAGCAGCTCCCATGGGGAAG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25.8; DB 1; Length 2334;
Pred. No. 8.8;
0; Mismatches 17; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 TGGGCTGCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
OCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patchaftn Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
ATORNET/AGENT INFORMATION:
NAME: KORD, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: UMO F
TELEPHONE: (810), 689-3500
                                                                                                                                                               3283 TCGTAGAAGCTGTTCCACAT 3302
                                                                                                                                      161 CTTGAAAGCTCTGCCTCCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (810) 689-3500
TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.38;
67.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2334 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 2316..2334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 67.99
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Michigan
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 48099
                                                                                                                                                                                                                                                  RESULT 13
US-08-406-070-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-08-406-070-1
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                                                                                                                                                                                                                       3223 CIGGGACTGATGCAGGCGTCCCGGTCACGGCCGACGGGGACTTCACCTACCGGGGACTT 3282
                                                                                                                                         3163 GACAGCCTTTCGCTGCACCACCTCTAGACACTGAAACGGAACGGGCCCTGTAGATGTTT 3222
                                                                                               41 GICCTCCTCITGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAA 100
                                                                                                                                                                                        101 CTGAAGCTGAAGGAGTCTTTTCTGACAAGTTCCTCCTATGAGTCCAGCTTCCTGGAATTG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 GICCICCICITGACCCICCTIGGCAGCICACAIGGAACAGGGCCGGGIAIGACTIIGCAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Geddel, David
APPLICANT: Lee, James M.
APPLICANT: Metchew, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
         / Match 14.7%; Score 26.4; DB 1; Length 4425; Local Similarity 49.3%; Pred. No. 7.3; nes 69; Conservative 0; Mismatches 71; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 14.7%; Score 26.4; DB 6; Length 4425; Best Local Similarity 49.3%; Pred. No. 7.3; Matches 69; Conservative 0; Mismatches 71; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
REPLICATION NUMBER: PCT/US95/04228
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             821P3PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILMS DATE: 04-APR-1994
ATTORING DATE: Wendy M. Lee
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 821P
TELECOMMUNICATION INFORMATION:
TELEPAN: 415/25-1994
TELEPAN: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 Dasses
                                                                                                                                                                                                                                                                                                           3283 TCGTAGAAGCTGTTCCACAT 3302
                                                                                                                                                                                                                                                                             161 CTTGAAAGCTCTGCCTCCT 180
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STRANDEDNESS: sing
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PCT-US95-04228-32
            Query Match
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; GENERAL INFORMATION:
APPLICANT: FUNDA, TSUNDA, TSUNDA, TSUNDA, TSUNDA, TSUNDA, TSUNDA, TSUNDA, TAMADA, TAMADA, TAMADA, TAMADA, TAMADA, TAMADA, TAMADA, TAMADA, TAMADA, TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN TITLES OF INVENTION: PARATHYROID HORMONE; NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: GUSHMAN
STREET: 130 Water Street
CITY: BOSTON
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.2%; Score 25.6; DB 1; Length 944; Best Local Similarity 54.2%; Pred. No. 6.9; Matches 52; Conservative 0; Mismatches 44; Indels (
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPALABLE
OPERATING SYSTEM: PC COMPALABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT PAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
FILING DATE: VOWER: US/08/665,617
FILING DATE: APPLICATION NUMBER: US/08/665,617
FILING DATE: NUMBER: US/08/665,617
FILING DATE: S31
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
RESERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATI
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COUNTRY: US
ZIE: 02109
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 CCGCGGGGTAGGAGCTGTGCGCACTCCCGATCTCCA 260
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
SADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
CITY: Florida
COUNTRY: USA
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
2.08-689-190-1
; Sequence 1, Application US/08689190
; Patent No. 5714349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-08-665-617-1
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96 CAATITIGITGCCTTAGGTGCCCCATIGGCTCCTCGTGATGCTGGTTCCCAAAGACCACG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 CCACTANGGGGTCTGGGCTGCCTCTTGACCCTCTTGGCAGCTCACATG 74
                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 7, 8, 9, 12, 15, 19, 21, 33, 36, 43, 51, 58, 60, ; IDENTIFICATION METHOD: S US-08-689-190-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.1%; Score 25.4; DB 2; Length 252; Best Local Similarity 56.6%; Pred. No. 4.5; Matches 47; Conservative 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: other nucleic acid, synthesizing DNA
Search completed: March 22, 2000, 01:22:37 Job time: 5641 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 TAAAAAGGAAGACAATGTCTTAG 178
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1..252
IDENTIFICATION METHOD:
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March 22, 2000, 05:09:44 ; Search time 802.03 Seconds (without alignments) 847.374 Million cell updates/sec
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180
1 CAGGAGGGCAGTGGCCACTA......CTTGAAAAGCTCTGCCTCCT 180
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4538634 seqs, 1887831982 residues
                                                                                                                 OM nucleic - nucleic search, using sw model
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em_est2:*
em_est2:*
em_est5:*
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em_est6:*
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Perfect score:
Sequence:
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0: 9b_est3 1: 9b_est3 2: em_est2 3: em_est2 5: em_est2 6: em_est2 7: em_est2 7: em_est3 9: 9b_est3 0: 9b_est3	61: 9D_est33:* 62: 9D_est33:* 64: 9D_est33:* 65: em_est23:* 66: em_est23:* 67: em_est23:* 68: em_est23:* 71: 9D_est41:* 72: 9D_est41:* 73: 9D_est41:* 74: 9D_est41:* 75: em_est23:* 76: em_est23:* 77: em_est13:* 77: em_est13:* 77: em_est13:* 77: em_est13:* 77: em_est13:* 77: em_est13:*	90.95.28.2 90.98.28.3 90.98.28.3 90.98.2 90.98.2 90.98.5 90.	11: em_gss/ 6: em_gss/ 7: em_gss/ 7: em_gss/ 7: em_gss/ 8: om_gss/ 9: of_gss/ 10: of_gss/ 10: of_gss/ 11: em_gss/ 12: of_gss/ 13: of_gss/ 14: of_gss/ 15: of_gss/ 16: of_gss/ 17: of_gss/ 18: of_gss/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AI857998 W169b01.x	AQ718761 HS_5511_B	AI136523 UI-R-C2p-	AQ290553 nbxb0037C	AW078074 fe24b05.v	AW128453 fe16b05.y	F08745 HSC1DB011 n
A	AI857998	AQ718761					
80	61	82	42	100	64	69	21
Query core Match Length DB II	404	552	328	268	537	523	339
Query Match	55.8	41.2	30.9	18.6	18.0	18.0	17.4
Score	100.4	74.2	55.6	33.4	32.4	32.4	31.4
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Result No.	O	O	υ	O	O	O	

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Enterior Service Chordata; Craniata; Vertebrata; Mammalia;
Enterior Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Entheria; Primates; Catarrhini; Hominidae; Homo.
Entheria; Primates; Catarrhini; Hominidae; Homo.
Enterior Canter Institute, Cancer Genome Anatomy Project (GGAP),
Noticonal Cancer Institute, Cancer Genome Anatomy Project (GGAP),
Tumor Gene Index
L Oppublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3189004.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Robert Strausberginih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CONA Catarribution: NCI-GGAP clone distribution information can be found through the I.M.A.G. E. Consortium/LiML at:
www-bio.llnl.gov/Dbrp/image/image.html
                                          AA38748 VC83407.11
AIJ79983 EST223714
AZ768084 EST223714
AZ768084 FF.3097_B
AZ996636 701546395
M89011 CELLAA7 Chr
AA094556 GSSTC-041
T41523 10104 Lambd
AA668276 ab78e11.s
AA76826 ab78e11.s
AA76826 bw60409.r
AA76892 vw60400.r
AA839043 vw60406.r
AA839043 vw60406.r
AA839539 UT-M-AN0-AIR81867 606744008
AW066263 687004408
AW066263 687004408
AW066263 687004408
AW066263 687004408
AW06263 687004408
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AQ647097 RPCI93-DP
AQ647978 RPCI93-EC
AA743733 CITEI-E1-
RQ9726 Y£27809.II
AT730173 BNLGHI586
AQ558186 hbxb0019H
AG50124 V2D2 mTn
T41525 10106 Lambd
        AA219322 zq17d07.s
AI730494 BNLGH1691
W70374 me15h03.rl
Z78408 HSZ78408 Hu
                                                                                                                                                                                                                                                                                                                                                                                                                          AI857998 404 bp mRNA EST 26-AUG-1999 wj69b01.xl NCI_CGAP_Lul9 Homo sapiens CDNA clone IMAGE:2408041 3',
                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                             AQ316270
AQ647097
AQ647978
AA774353
AQ473733
R09726
                                                                                                                                                                                      AI881867
AL117984
AW066022
AW066263
AO527267
AQ613185
AI727080
AI730002
                                                                                                                                                                                                                                                                                                                     AI730173
AQ258186
AQ500124
T41525
                                                                                 M89011
AO904556
T41523
T41535
                                              AA387480
AI179983
AQ768084
AI998636
                                                                                                                                                           AA839043
AI463192
AI839539
T41524
AA219322
AI730494
W70374
                                                                                                                      AA668276
AA716892
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AIB57998
AIB57998.1 GI:5511614
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/organism="homo sapiens"
/db_xref="taxon:966"
/db_xref="taxon:966"
/clone="InAGE:1408041"
/clone=lib="Nx1_CAbe_Lul9"
/tissue_lype="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
metastatic)"
/dev stage="adult"
/lab_host="bhi08" (phage-resistant)"
/note="organ: lung; Vector: pT/T3D-pac (Pharmacia) with a
modified pOlylinker; lst strand cDNA was prepared from
pooled lung tumor tissue, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT/T3 vector. Library went througb one round of
normalization. Library constructed by Bento Soares and M.
Fatima Bonaldo.

97 a 105 c 117 g 84 t 1 others
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue Morth, Seattle, WA 98109, USA
Tel: (206) 616-3888
Fax: (206) 616-38887
Email: Jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pleter de Jone
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (fifo@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1087 row: L column: 18
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Mahairas,G.G. Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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HS_5511_B2_F09_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1087 Col=18 Row=L, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 CAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAGTTCCTCT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 CAGGGCGGGTATGATTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAATTCCTCT 252
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.8%; Score 100.4; DB 61; Length 404; 98.1%; Pred. No. 6.7e-21; clive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 AIGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 ATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTNTGCCTCCT 209
Seg primer: -40UP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
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AQ718761.1 GI:5468077
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Matches 101; Conservative
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                                                               FEATURES
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/organism="Rattus norvegicus"
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="texn:10116"
/clone="IU-R-C2p-nq-e-02-0-UI"
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/note="Vector: prT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoarcestblue.weeg.ulowa.edu
The sequence tag present in the cDNA between the NotI site and the
Oligo-dr track served to identify it as a clone from the normalized
adult Lung library. CDNA Library Preparation: M. Fatima Bonaldo.
Ph.D. Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 121: 319 335 8256 Fax: 319 335 9256
                                                                                                                                                                                            /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 153 c 124 g 117 t 17 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 PACAGGGCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAGTTCCTC 135
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.
1 (bases 1 to 328)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Jan 19, 1998 this sequence version replaced g1:2150222. Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                        Query Match 41.2%; Score 74.2; DB 82; Length 552; Best Local Similarity 85.4%; Pred. No. 8.7e-13; Matches 82; Conservative 0; Mismatches 14; Indels 0
                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=1087 Col=18 Row=L"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 CTATGAGTCCAGCTTCCTGGAATTGCTTGAAAGCT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
Seq primer: T7
Class: BAC ends
High quality sequence stop: 552.
Location/Qualifiers
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Location/Qualifiers
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Rattus norvegicus
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mixture of individually tagged normalized libraries maxture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18 day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UTR-C2D) was constructed as follows: PCR amplified cDNA inserts from UTR-C1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UTR-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UTR-C2 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Lillopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ290553 568 bp DNA GSS 03-DEC-1998 nbxb0037C20f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0037C20f, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 TGACAAGTICCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 AGGCCAAGACCTCCCAAGACTCCGGCTTCTGGACATGCTCCAAAGATCTGCCTCCT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poaceae; Oryza.
1 (bases 1 to 56)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 30.9%; Score 55.6; DB 42; Length 328; 1. Similarity 66.9%; Pred. No. 3.8e-07; 79; Conservative 0; Mismatches 39; Indels 0;
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/db_xref="taxon:4530"
/clone="nbxb0037C20f"
/clone=lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
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Clemson University
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    . 568
    /organism-"Oryza sativa"
    /strain-"Japonica"

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High quality sequence stop: 317.
Location/Qualifiers
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SM Danio rerio

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Eukaryota; Tuteloosta; Euteloosta; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinides; Rasborinae; Danio.

1 (Dasea I to 523)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,R., Stepfoce,M., Theislang,B., Allen,M., Bowers,Y.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
Washu Zebrafish EST Project 1998
Unpublished (1989)
On Dec 20, 1995 this sequence version replaced gi:ll34195.
Other_Esrs: fel6b05.xl
Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alab host "Xil-blue MR"

// Jab host "Xil-blue MR"

// Jab host "Xil-blue MR"

// Iab host "Xil-blue MR"

// Is Strand CDNA was primed with a Nct I - oligo(dT)15 primer

// Is pranded CDNA was ligated to Sal I adaptors (BRL),

digested with Nct I and cloned into the Nct I and Sal I

sites of the pSPORTI Vector (BRL). Library was constructed

by Matthew Clark (Lehrach lab; ICRF, London and Max Planck

Institut fuer Molekulare Genetik, Berlin). CDNAs for EST

analysis were selected following oligonucleotide

hybridization ingerprinting of arrayed clones from

abrafish late somitogenesis (26 ss), adult liver or

embryonc shield steps (5.6 h) libraries. Fingerprint

deta were used to computationally cluster cDNAs, and a

single CDNA from each cluster was chosen for sequencing.

In some cases multiple members of the same cluster were

sequenced to assess clustering parameters or single clones

were sequenced additional times to assess quality
             RessourcenterumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
Seq primer: B from Amersham
High quality sequence stop: 498.
Location/Qualifiers
                                                                                                                                                                                                                         1. .537
/organism="Danio rerio"
/db_xref="taxon:7955"
/db_xref="taxon:7955"
/dc_lb_"Zebrafish WashU MPIMG EST"
/sext="aixed"
/tissue_type="26 somite embryos, adult livers, shield
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fel6b05.yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5', mRNA
sequence.
AW128453.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.0%; Score 32.4; DB 64; Length 537;
ilarity 56.6%; Pred. No. 6.3; Conservative 0; Mismatches 46; Indels 0;
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Matches 60; Conserv
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AW128453/c
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/lab_host="E. coll DH10B"

//abc_host="E. coll DH10B"

//acce="vector: pBeloba61]: Site_1: HindIII; Site_2:

//Anote="vector: pBeloba61]: Ale_1:

// Anote="vector: pBeloba61]: Ale_1:

// Anote="vector: pBeloba61]: Ale_1:

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fe24b05.yl 2ebrafish WashU MPIMG EST Danio rerio cDNA 5', mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480 GGACGACCTGCGGAAGAATTTAGGCTGCCGTTTCTGCCCAGGGCCGGCTTCGA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAGTTCCTCTATGA 141
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AW078074.1 GI:6033226
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AW078074/c
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Gaps

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/BSLA Fyendal brain"

/dev_stage="3 moths old"
/dev_stage="3 moths old"
/note="Corgan: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: Noti; sea=Female; dev_stage=3 months old;
Isolate=muscular atrophy patient; tissue_type=total
brain; total manA was olioo; dir primed and directionally
cloned 5' -> 3' into the HindiII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, PN.A.S in press;
57 a l16 c 100 g 64 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newman, T., deBruijn, P.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, Of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thale cress.
Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Magnollophyta; eudicotyledons; core
eudhyllophytes; Spermatophyta; Magnollophyta; Erassicaceae;
                     Devignes, M.D., Duprat, S., Roulgatte, R., Jumeau, M.N., Lamy, B., Caranzo, F., Mitchell, H., Marthage-Samson, R., Pletu, G., Poullot, Y., Sobastiani Rabaktchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10105 Lambda-PRL2 Arabidopsis thaliana cDNA clone 100A7T7, mRNA Sequence. T41524 GI:9931185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genexpress_library_idt: C; Genexpress_sequence_idt: y3c-ldb01
Seq primer: (-21)M13_universal
High quality sequence stop: 277.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  Genethon Centre de recherche sur le Genome Humain
1. Lue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
1. 131: 33160778698
Fax: 33160778698
                                                                                                                                                                                                                                                                                          On Sep 21, 1992 this sequence version replaced gi:279421 Contact: Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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/db_xref"taxon:9606"
/clone="c_idb0l"
/clone="lib="normalized infant brain cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genexpress@genethon.fr
Single read.
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1 (bases 1 to 545)
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Exa: 314 286 1800
Exail: zbrafish@watson.wustl.edu
CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
MAtthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center clone distribution: Genome Systems, St. Louis,
Miscouri (web address: www.genomesystems.com) (enail contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact:
info@genomesystems.com) (email contact:
info@fenomesystems.com) (e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="26 somite embryos, adult livers, shield stage embryos"
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MSC1DB011 normalized infant brain cDNA Homo sapiens cDNA clone
c-1db01, mRNA sequence.
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Butherial, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 339)
Auffray.C., Behar,G., Bols.F., Bouchier,C., da Silva,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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/db_xref="taxon:1955"
/clone_lib="zebrafish WashU MpIMG EST"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 t
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Seg primer: T3 ET from Amersham
High quality sequence stop: 488.
Location/Qualifiers
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es 60; Conserv
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Genome Res. 6 (9), 807-828 (1996)

5 97044478

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: est@wastson.wustl.edu
This clone is available royalty-free through LLML; contact the
TMAGE Consortium (inf@@image.lln1.gov) for further information.
Seq primer: -41m13 fwd. Er from Amersham
High quality sequence stop: 389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gestyplum historium
Gestyplum historium
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Eudicotyledons; core
eunphyliophytes; Spermatophyta; Majonliophyta; eudicotyledons; core
eudicots; Rosidae; eurosida II; Malvales; Malvaceae; Gossyplum.

I (bases I to 589)
Blewitt,M., Matz,B.C., Davy,D.F. and Burr,B.
ESTS from developing cotton fiber
Onpublished (1999)
On Dec 4, 1997 this sequence version replaced g1:2522479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI730494 589 bp mRNA EST 11-JUN-1999
BNIGH16911 Six-day Cotton fiber Gossypium hirsutum CDNA 5' sinilar
to (AF608122) alpha-tubulin 3 [Eleusine indica], mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTT 121
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Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burrébnlux1.bnl.gov
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1 (bases I to 427)

1 (bases I to 427)

1 (bases). Lemnon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisaoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hankins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Le, M., Mardis, E., Moorte, B., Morria, M., Parsons, J., Prange, C., Rifkin, L., Tieveskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA219322 427 bp mRNA EST 07-FEB-1997 zq17d07.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629965 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 TTTTCTGACAAGTTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                        Contact: Thomas Newman
MSU-DDE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                        On Jan 24, 1995 this sequence version replaced gi:634112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.2%; Score 31; DB 23; Length 545; 52.9%; Pred. No. 17; tive 0; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 others
                                                                                                                             Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Insert Length: 643 Std Error: 0.00
Seq primer: T7 dye primer
High quality sequence stop: 369.
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Plant Physiol. 106, 1241-1255 (1994)
95148729
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Location/Qualifiers
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HSZ78408 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone
3.99 (CEPH), mRNA sequence.
278408 GI:1495181
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1 (bases I to 742)

Neri,C., Albanese,V., Lebre,A.S., Holbert,S., Saada,C., Bougueleret,L., Meier-Ewert,S., LeGall,I., Millasseau,P., Bul,H., Glud,Celli,C., Massart,C., Guillou,S., Gervy,P., Poullier,E., Lehrach,H., Cohen,D. and Cann,H.M.

Survey of CAG/CTG repeats in human cDNAs representing new genes: candidates for inherited neurological disorders

96414310
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/db_xref="taxon:9606"
/clone="3.99 (GEPH)"
/clone=11b="Human fetal brain S. Meier-Ewert"
//tssue_type="brain"
/dev_stage="fetus"
/note="cDNA library of S. Meier-Ewert, Max Planck
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                                                                                                                                                                                                                                                                                          DB 26; Length 392;
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232 c 215 g 131 t l
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27 Rue Juliette Dodu, 7510 Paris, France
ICRF clone ID ICRFp507L04199.
Location/Qualifiers
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Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 392)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Leh., Marrin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W70374 392 bp mRNA EST 17-JUN-1996 mme15h03.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:387605 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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The WashU-HHMI Mouse EST Project
Unbublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="texon:10090"
/clone="ImAGE:387605"
/clone_lib="Soares mouse embryo NDMEl3.5 14.5"
                                                                                                                                                                                                                                                                                                          DB 51; Length 589;
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           Location/Qualifiers

1. 589

Organism="Gossypium hirsutum"

(oultivar="Acala Maxxa"

(db_xref="taxon:585"

(clone_lib="51x-day Cotton fiber"

/tissue_type="immature fiber"

/dev_stage="$1x days post anthesis"

/lab_nost="Xil" Blues

/lab_lost="Yestor: pBluescript II KS+"

foote="Vector: pBluescript II KS+"

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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                          Score 30.8; DB
Pred. No. 20;
0; Mismatches
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il Similarity 61.0%;
50; Conservative (
Seg primer: T3 Primer
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REFERENCE AUTHORS

TITLE JOURNAL

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AI179983 524 bp mRNA EST 20-JAN-1999 ESI223714 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone RSPC049 3' end, mRNA sequence.
AI179983.1 GI:3730621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp.

Rattus sp.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

Les, W. H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,

Rat Genome Project: Generation of a Rat EST (REST) Catalog 6 Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Normalized rat spleen, Bento Soares"
/note="organ: spleen; Vector: pT7T3Pac; Site_l: EcoRI;
Site_2: NotI"
1 124 c 141 g 130 t
                                                                             57 TCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-818-5529 Tel: (301)-818-0508 Email: nhlee@tigr.org Seq primer: M13-21.
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1. .524
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. /organism="Rattus sp."
/db_xref="ATCC (inhost):2035352"
/db_xref="texon:10118"
/clone="RSPC049"
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AQ768084.1 GI:5646200
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Unpublished (1998)
Contact: Lee, NH
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Salael, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

In Washu-HHMI Mouse EST Project
Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1317023.

Contact: Marza M/Mouse EST Project
Washington University School of Medicinep (Washington University School of Medicinep (Tel: 314 286 1810)

Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
MGI:474021
High quality sequence stop: 81.
Location/Qualifiers
1. 290
/organism="Mus musculus"
/gtrain="C57BL/61"
Gaps
                                                                                                                                                                                                                                                                                                                           AA387480 290 bp mRNA EST 23-APR-1997 vc83d07.r1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone IMAÇE:789613 5', mRNA sequence.
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AA387480.1 GI:2040672
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Local Similarity 61.2%;
Nes 49; Conservative
                                                                                              93 CTTTGCAACTGAAG 106
                                                                                                                                                                 303 ACTTICANCIGNAG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse
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FEATURES

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Gaps

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Query Match Best Local S Matches 49

BASE COUNT ORIGIN

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Hood, L. Sequence approach to mapping and scanning the human genome readged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

By 99390599 Secondaric Mahairas GG, Wallace JC, Hood L. High Throughput Sequencing Center University of Washington North, Seattle, WA 98109, USA Tel: (206) 616-3887

Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 3097 row: J column: 21
Seq primer: M13 Reverse
Clones may be purchased from Sesearch Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 3097 row: J column: 21
Seq primer: M13 Reverse
Closs: BAC ends
High quality sequence stop: 445.

Location/Qualiflers

Location/Qualiflers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 445)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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16.9%; Score 30.4; DB 87; Length 445;
Best Local Similarity 67.2%; Pred. No. 24;
Matches 43; Conservative 0; Mismatches 21; Indels 0;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

50: gb_pl3:*

SUMMARIES

us-09-092-296-2.rge

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

- nucleic search, using sw model nucleic

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March 21, 2000, 14:39:02; Search time 479.47 Seconds (without alignments) -1450.209 Million cell updates/sec US-09-092-296-2 229 1 ACCGGGACIICAGIGICICC.......CCAICICCCIICAGGACCA 229 1642386 821193 segs, -1518192014 residues pass the threshold gb_bal:* gb_om:* gb_om:* IDENTITY_NUC GenEmb1:* Number of hits that 0 Title: Perfect score: Sequence: Scoring table: Word size : Database : Searched: Run on:

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gb_ph: *
gb_p11: *
gb_p12: *

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em_hun:*
em_hun!:*
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em_non:*
em_pri:*
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AB023048 192650 bp DNA PRI 20-NOV-1999
Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
Colone:35L9, complete sequence.
AB023048
AB023048.1 GI:5672603 for sapiens cell_line:978SK DNA, clone:53L9.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo. ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION RESULT AB023048 LOCUS

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project of JST
Japan Science and Technology Corporation (JST)
Japan Science and Technology Corporation (JST)
5-3, Yonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan
For further information about this sequences, please visit our
aequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.
html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
Location/Qualifiers
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Homo sapiens clone UMGC:370M23.002 from 6p21, complete sequence.
AC005937
AC005937.1 GI:3845393
HTG.
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47.8%; Score 109.4; DB 10; Length ;
Best Local Similarity 95.0%; Pred. No. 2.9e-24;
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S Shinas, 7. Tamiya, G., Oka, A. and Inoko, H.
Homo sapiens 2,229,818Bp genomic DNA of 6p21.3 HLA claas I region
Homo sapiens 2,229,818Bp genomic DNA of 6p21.3 HLA claas I region
Homo sapiens 1 to 200000)
E 2 (bases 1 to 200000)
S Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
Direct Submission
L Direct Submission
L Science and Technology Corporation (JST), Advanced
Hirakawa, Japan Science and Technology Corporation (JST), Advanced
Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
UNLI https://www-alis.tokyo.jst.go.jp,
Fax:81-3-5214-8491,
This sequence is conducted by Tokal University as a JST sequencing
                                  Shinna,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
Watanabe,R., Fukuzumi,Y., Itakura.S., Sugawara,C., Ono,A.,
Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahram,S. and Inoko,H.
Molecular dynamics of MHC genesia unraveled by sequence analysis of
the 1,796,938-Bp HLA class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
                                                                                                                                                                                                                                       Journal To 192650)
Shiina T. and Takishima, N.
Shiina T. and Takishima, N.
Direct Submission Submitted (29-JaN-1999) to the DDBJ/EMBL/GenBank databases. Takashi Submitted (29-JaN-1999) to the DDBJ/EMBL/GenBank databases. Takashi Shiina, Tokai University School of Medicine, Department of Molecular Life Science 2; Bohneidal, Isehara, Ranagawa 259-1193, Japan (E-mail:tahina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884)
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Phone:+81-463-93-1121, Fax:+81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
47.8%; Score 109.4; DB 10; Length 192650;
Best Local Similarity 95.0%; Pred. No. 2.9e-24;
Matches 113; Conservative 0; Mismatches 6; Indela 0; G
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Homo sapiens genomic DNA,
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AP000511.1 GI:5926698
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/note="clonal variation with 3' overlapping clone" 47240. 47256
/note="clonal variation with 3' overlapping clone - insertion of 17bp repeat" a 11489 c 12284 g 11994 t
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44451
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44337
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45900
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46851
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                                                                     /sub_clone-"UWGC:370M23.002"
Cflone-lib-"Research Genetics BAC Library"
3647. .3932
/rpt_family-"alu"
                                                                                                                                                                                                                                                                                            complement(8164. .8609)
/rpt_family="alu"
complement(21287. .21895)
/rpt_family="alu"
22715. .22957
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                               complement(4999. .5277)
                                                                                                                                                                                                    /rpt_family="Alu"
complement(6972, 7050)
/rpt_family="MLT1"
                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Alu"
27835. 28010
/rpt_family="MBR20"
31295. 315.
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40046. .40156
/rpt_family="Alu"
43194. .43372
43325
43325
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38526. .38700
/rpt_family="MER3"
39583. .40010
                                                                                                                                                                                                                                                                      /z86. ./264
/rpt_family="Alu"
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15510. .25802
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/rpt_family-"Alu"
33515. .33767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14223. .34290
'rpt_family="MIR"
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Validation:
This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.
  SM Homo sapiens
Eutheria: Primates; Catarrhini; Hominidae; Homo.
Eutheria: Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 4732)
S Jamer, M., Guillaudeux, T., Vu,Q., Kutyavin,T., Harter,H. and Geraghty,D.E.
Large scale sequence analysis of the human MHC class I region Unpublished (1989)
Fred Hutchinson Cancer Research Center
The Clinical Research Division
1100 Fairriew Ave. N., P.O. Box 19024
Seattle, MR 98109-1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                Direct Submission
Submitted (05-NOV-1998) Human Genome Center, University of
Washington, Box 352145, Seattle, WA 98195, USA
University of Mashington Human Genome Center
Box 352145 Seattle, WA 98195
Contact: Daniel E. Geraghty (geraghty@fhorc.org)
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5': UWGC:370m23.013 (Genbank Accession: AC005530)
3': UWGC:y67cil2 (Genbank Accession: AC004211)
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DS or two chemistry coverage:
Single stranded regions:
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RESULT 4 HSDJ144C9/C

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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mount of special metazoa; Chordata; Craniata: Vertebrata; Mammalia; Eukaryota: Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 211190)
Waterston. R. H.
The sequence of Homo saplens clone
Unpublished
2 (bases 1 to 211190)
Waterston. R. H.
Direct Submission
Submission
Submission
Oniversity School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108; USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC016716 211190 bp DNA HTG 04-DEC-1999
Homo sapiens clone RP11-31213, *** SEQUENCING IN PROGRESS ***, 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DD 31300 TGTTGCCTCCCTCCAGGATCCCTTTGGTGAGTATGGTGTTCAGGATGCACCACCACCAC 31241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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Center project name: H_NH0312103.

**NOTE: This is a "working draft" sequence. It currently

**consists of 31 contigs. The true order of the pleces

**is not known and their order in this sequence record is

**arbitrary. Gaps between the contigs are represented as

**runs of N, but the exact sizes of the gaps are unknown.

**This record will be updated with the finished sequence

**as soon as it is available and the accession number will

**be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.0%; Score 34.4; DB 10; Length 77322; Best Local Similarity 63.1%; Pred. No. 1.7; Matches 53; Conservative 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2127: contig of 2127 bp in length 2145: gap of unknown length 4245: contig of 2081 bp in length 4244: gap of unknown length 6447: contig of 2203 bp in length 6465: gap of unknown length 9092: contig of 2627 bp in length 9110: gap of unknown length 11195: contig of 2085 bp in length 11213: gap of unknown length 11213: gap of unknown length 14033: contig of 2820 bp in length 14051: gap of unknown length
                                                                                                          /note="match: GSS: Em:AQ307331"
complement(24637, 25031)
/note="match: GSS: Em:AQ234890"
27999, 28360
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Direct Submission

Submitted (22-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Nov 22, 1999 this sequence version replaced gi:613875.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlapping clone, as we submit sequences with
only a small overlapping clone, as we submit sequences with
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1. constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RPI-14409 is from the library RPGT-1 constructed at the Roswell RPAT-14409 is from the library RPGT-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Enr. EMBL: Sw., SWISSEROT; Tr., TREMBL: WORWPEP; Information on the WORWPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                           HSDJ144C9 77322 bp DNA PRI 22-NOV-1999
Human DNA sequence from clone RP1-144C9 on chromosome 1p34.3-36.11,
complete sequence.
      ö
                                                                                          Db 35121 ACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCACTATGGGGGTCTGGGGT 35180
                                                                                                                                                                                                        DD 35181 GCCCCTTGTCCTCCTTGACCCTCCTTGGCACACGGAACAGGTGAGGGCTAGA 35239
      Gaps
                                                           8
                                                                                                                                                                               61 GCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 77322)
Hall, R.
                                                                 1 ACCGGGACITCAGTGTCTCCICCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT
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Location/Qualifiers
      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2858. .3151
/note="match: GSS: Em:AQ627537.1"
complement(11439. .11580)
/note="match: GSS: Em:AQ031787"
complement(24560. .25030)
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/hote="match: 68S: Em+Aq335665"
complement(1780 .2227)
/hote="match: 68S: Em+Aq355618"
      Mismatches
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/db_xref-"taxon:9606"
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/map="p34.3-36.11"
/clone="RP1-144C9"
/clone_11b="RPCI-1"
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL096774.9 GI:6465842
      Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
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FEATURES

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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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                                            RESULT
AC016764
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OSU25430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 GACTITGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTT 177
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contig of 3080 bp in length gap of unknown length contig of 2431 bp in length contig of 2238 bp in length gap of unknown length length lengthl
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gap of unknown length
contig of 26277 bp in length.
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52007 c 53208 g 52618 t
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/db_xref="taxon:9606"
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20581
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22855
25614
27882
27900
32616
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36104
40578
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44563
48844
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72141
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97309
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Direct Submission

La Submitted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA

Mo 63108, USA

On Dec 10, 1999 this sequence version replaced g1:6524275.

Center project name: H_NH0549G13.

* NOTE: This is a "working draft' sequence. It currently toners for a "working draft' sequence. It currently toners from and their order in this sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
AC016764 191010 bp DNA HTG 09-DEC-1999
Homo sapiens clone RP11-549G13, WORKING DRAFT SEQUENCE, 1 unordered
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 148331 CCAGGCCTTCCTCAGAGGCATGTGACTCACCTGTGTCCCTCCACCCTGCCAGCTG 148390
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Oryza sativa nucleotide pyrophosphatase precursor, mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 148271 GCAGAACCTIGCTCCCTGCCACCACTGGGAGCTGGCACAAGCCCCAGTGGAG 148330
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                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Frimates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 191010)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.0%; Score 34.4; DB 45; Length 191010; 50.6%; Pred. No. 1.7; Live 0; Mismatches 81; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 191010: contig of 191010 bp in length.
Location/Qualifiers
1. .191010
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-549G13"
46669 a 48592 c 47516 g 47765 t
                                                                                                                                                                                                                                                                                                                                                                    The sequence of Homo saplens clone Unpublished
                                                                                          AC016764
AC016764.2 GI:6554041
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 191010)
Waterston, R.H.
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Best Local Similarity 50.69
Matches 83; Conservative
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U25430.1
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LE Submitted (35-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone-quest@sanger.ac.uk
CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone-quest@sanger.ac.uk
On Jul 27, 1999 this sequence version replaced gi:5579004.
Outing sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
EMT. SWT. SWTSSPROT, TT., TREMEL, WP., WORWEPP, Information
on the WORWEPP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats but not necessarily within known
annotated human repeat sequence elements (e.g. Alu), where the
sequence is ambiguous, there is an annotation using the 'unsure'
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                                                                            HSJ858BL6 36676 bp DNA PRI 23-NOV-1999
Human DNA sequence from clone 858Bl6 on chromosome 22. Contains the RIANO542 gene and a gene for a novel protein similar to hamster PSSC (Phosphatidylsearine Decarboxylase Proenzyme, EC 4.1.1.65).
Contains ESTs, GSSs and a putative CPG island, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(<273. .454,1413. .1488,1978. .2073,2538. .2614,
3997. 4099,5606. .5702,8812. .8972,9435. .9599,10811. .
11023. .11197,11271. .11524,12717. .12948,14414. .14546,
14669. .14147,12784. .15895,15983. .16217)
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The true left end of clone 694E4 (AL031255) is at 36572 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 36676)
Barlow, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: ESTs: Em:R53362 Em:Z78408 Em:AA521233
                                                                                                                                                                                                                                                                                                                      ALO96768.7 GI:5596770
HTG; CpG Island; KIAA0542; Phosphatidylserine Decarboxylase
Proenzyme; PSSC.
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/db_xref="taxon:9606"
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/clone_lib="RPCI-5"
/clone="RP5-858B16"
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            RESULT 8
HSJ858B16
LOCUS
DEFINITION
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VERSION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
Posceae; Oryza.

1 (sites)
Hsing,Y.C., Tsao,C.V., Chow,T., Hsieh,J. and Chen,Z.
Rice early embryogenesis gene
Unpublished
2 (bases 1 to 1801)
Hsing,Y.C.
Direct Submission
Submitted (20-APR-1995) Yue-ie C. Hsing, Academia Sinica, Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //CERIS LA COR-"MARAAAAPPPRAAGDSPPPTALLLPRITTTAGAAPAPRRSSAS
SRHILLITAALAVATSYLLILERIPLSAAPAAAARAQVKLEKPVVILISSDGFRF
GYOHRAATPHIRKLIGNGTSAAFACALOFPFPHYSTPPHYSTS ATGLIPPSHSSHSTINKPPP
PISGDFTMSSRPFRWHGEPLWYTAADGGLQAATFWFGSSFVRGSWDCPBYYCRHY
NGSVPFEERVDALLGYFDLPSDEMPQFLILIFEDPDHQGHQVGPDDPAITEAVVRIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIGRLIAGLEERGVFEDVNYILVGDHGWYGTCDKKIVFLDELAFWIKLEEDWYLSKTP
LLAIRPPDDMSLPDVVAKMNEGLGSGKVENGEYLRMYLKEDLPSRLHYADSYRIPPII
GLPEEGYKVEMKRSDKNECGGAHGYDNAFFSNRTIPIAHGPRPEGGRVVPSFENVEIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="3 to 5 days after anthesis" 
/clone_llb='constructed by Y.C. Hsing et al., Academia
Sinica, Institute of Botany, Taipei, Taiwan, 11529,
Republic of China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 AAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 TIGACCCTCCTIGGCAGCTCACAIGGAACAGGGCCGGGTAIGACITIGCAACIGAAGCIG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GAGAAGCCGGTGGTGATCCTCTTCTCCTCCGACGGGTTCCGCTTCGGGTACCAGCACAAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö

    .96
    /note="signal peptide to endoplasmic reticulum"

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/product="nunleotide pyrophosphatase precursor"
/protein_id="AAA67067.1"
/db_xref="GI:818849"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.8%; Score 34; DB 7; Length 1801; 48.0%; Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40. 1479
/EC_number="3.6.1.9"
/note="nucleotide phosphodiesterase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="early embryos in seeds" 40. .96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVIASILNLEPAPNNGSSSFPDTILLPSE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa"
/strain="Tainung 67"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 9
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1572. .1576
/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGCCTCCTCCATCTCCC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GCGCGACCCGCACATCCACC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="0SE4"
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les 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       china
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                                                                                                                                                         JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
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JOURNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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19703. 123441,15318. 12534,11333. 121340,23432. 123003, 28473. 28484)

/gene="dd588B16_2"
//Octe="match: CDN48: Em:M62722 Em:AL050371 Em:AF086277
Em:AR32439 Em:AR66212 Em:AR011114; match: E5TS:
Em:AR32439 Em:AR68212 Em:AR011114; match: E5TS:
Em:AR32439 Em:AR68212 Em:AR01114; match: E5TS:
Em:AR32439 Em:AR673371 Em:AR01935 Em:AR18158
Em:AR371291 Em:AR337672 Em:AR051210 Em:AR39268
Em:AR4717291 Em:AR337672 Em:AR05131 Em:AR397077 Em:AR39208
Em:AR4717291 Em:AR37754 Em:AR0603 Em:AR496707 Em:AR643609
Em:AR401352 Em:AR37754 Em:AR397076 Em:AR496707 Em:E1002
Em:AR01135 Em:AR397754 Em:AR19982 Em:AR496707 Em:R51102
Em:R403173 Em:AR397754 Em:AR19983 Em:R49393
Em:R403173 Em:AR397754 Em:AR191787 Em:AR39933
Em:R403173 Em:AR397184 Em:AR191798 Em:R493093
Em:R403173 Em:AR39254 Em:AR39784 Em:R77685
Em:R6936 Em:R6936 Em:AR39566 Em:AR395719 Em:AR39739 Em:AR3993 Em:AR3993 Em:AR3993 Em:AR3993 Em:AR3993 Em:R889234 Em:AR3993 Em:AR3994 Em:AR3993 Em:AR3993 Em:AR3999 Em:AR39999 Em:AR3999 Em:AR3999 Em:AR3999 Em:AR3999 Em:
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                                                                                       7.010-1.103.

7.010-1.103.

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7.010-1.103.

7.010-1.103.

7.010-1.103.

7.010-1.103.

7.010-1.103.
            1650. 4754
note="AluSg/x repeat: matches 200. .307 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"MIR repeat: matches 46. .208 of consensus" 1305. 13779
/note-"L2 repeat: matches 1570. .2750 of consensus" 15108. .15404
/note-"Lauga repeat: matches 1. .295 of consensus" complement(16160)
/gene-"dJ858816.2*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.8%; Score 34; DB 11; Length 36676; 54.9%; Pred. No. 2.1; tive 0; Mismatches 55; Indels 0
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                repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence-not_experimental
product="44858816.1.1 (KIAA0542 (1550zm 1))" 214,
join(<273...454,1413...1488.1978...2073,5238...2514,
3997...4099,5606...5702,8812...8972,9435...9509,10811...10885,
11023...11199,11271...12948.14414...14546,14669...14747,
15784...15895,15983...16218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .10885,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence-not_experimental
/product="d185816.1.2 (KIAA0542 (Lsoform 2))"
/product="d185816.1.2 (KIAA0542 (Lsoform 2))"
/protein_id="c185931"
/db_xref="d1:5921490"
/translation="QAILHAREROLLYRSWFWWHOQAARHQEOEWQTVACAHRRGRL
KKAFCCHRESAGGLERERTGRYRAARERHAAQLLRRWRGAGTARARAC
LHHGHSYLHRRALQAWTYOGRYRSILAEWAARESOHHRQLLRGALRRWRSWTMARAVD
AKKIFQASTHYRRIICSKYLVQWREAVSVQWYYRQOEDCAIWBAQKULDRGCLRTWFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWDCSRRSAQQRLQLERAVQHHRQLLLEGIARWTHHLQCYRKRLLHRQSTQLLAQ
RLSRCFRQWRQQLERRRQBQRAYVRALWFRSESLQAKWATHLAFTLERRKKRALQ
WALQAYOGQULLGGATRLLERASWRSSRQQLQAQQOVQAABSLHRAVRRATLWQR
VLGRGGRPQPLAAIAPSRKVTFEGPLINRIAAGAGOGTLETKRPQASSPLGALGRLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      //octe-"original published form; could be artefactual as it
fis result of a large intron read-through; match: proteins:
Tr:060289"
Em:AA673371 Em:AI190893 Em:AI019759 Em:AI770152
Em:AA149582 Em:N30173 Em:A1342072 Em:R54847 Em:AI126154
Em:AA118158 Em:AA044044 Em:N54928 Em:AA315892 Em:AA398600
Em:AI623440 Em:AI024124 Em:AA637284 Em:AI842779
Em:AI094871 Em:AI192647 Em:N63934 Em:AV083921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         John (<273. .454,1413. .1488,1978. .2073,2538. .2614, .709,2016. .2073,2538. .2614, .709,297. .4099,5606. .5702,8812. .8972,9435. .9599,10811. .11023. .11199,11271. .11544,17717. .12948,14414. .14546, .14669. .14747,15784. .15895,15983. .16087) .700te="40388816.1" .700te="40388816.1" .100 published protein but supported by FGENES and GENSCAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: GSS: Em:A0545234"
3250. .3536
/note="AluJo repeat: matches 2. .302 of consensus"
3634. .3836
/note="L2 repeat: matches 2497. .2701 of consensus"
4356. .4646
/note="laluSx repeat: matches 21. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     620. .913
/note="AluSx repeat: matches 1. .294 of consensus"
1444. .167.
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                                                                                                                                                                                                                                                                                                                                                          /note="match: cDNAs: Em:AB011114"
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/product="d1858B16.1.2 (KIAA0542 (isoform 2))"
273. .16218
/gene="dJ858B16.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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1 (bases 1 to 291288)

12 (bases 1 to 291288)

13 (bases 1 to 291288)

14 (bases 1 to 291288)

15 (bases 1 to 291288)

16 (10-Add-1999) Production Sequencing Facility, DOE Joint Genome Institute.

200 Mitchell Drive, Walnut Creek, CA 94598, USA On Oct 31, 1999 this sequence version replaced gi:5686195.

** WOTE: This is a "working draft' sequence. It currently consists of 160 contigs. The true order of the pieces are in of known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as a soon as it is available and the accession number will be preserved.
ACUU8878 291288 bp DNA HTG 31-OCT-1999
(* Homo sapiens chromosome 19 clone CITB-HI_2207023, *** SEQUENCING IN PROCESS ***, 160 unordered pieces.
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Center: Whitehead Institute/ MIT Center for Genome Research
                                     AC016298 62181 bp DNA HTG 24-NOY-1999
Homo sapiens clone RP11-655M17, LOW-PASS SEQUENCE SAMPLING.
AC016298 1 GI:6467036
HTG: HTGS_PHASEO.
                                                                                                                                                                                                 * NOTE: This record contains 78 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submission@enome.wi.mit.edu
Center: Project Information
Center project name: 14315
Center clone name: 655_M_17
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0; Mismatches 75; Indels 0;
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of 1344 bp in length
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of 1035 bp in length
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6393	7995	8803	9604	10401	11207	12025	12841	13638	14441	15235	16032	16837	17616	18422	19234	20043	20857	21658	22463	23263	24066	24867	25674	26476	27271	28076	28818	29614	30417	31208	32022	32826	33592	34404	
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contig of 809 bp in length gap of unknown length contig of 807 bp in length gap of unknown length contig of 802 bp in length gap of unknown length contig of 797 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length	of 829 bp 1n on known lengt on Known lengt on 682 bp 1n o	TO PER SOLUTION OF THE PROPERTY OF THE PROPERT
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repeat: matches 76. .206 of consensus"

Db 12025 GCCTCGGGTTGCA 12037

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Direct Submission

Submitted (10-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mall enquiries: humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk

On Jul 27, 1999 this sequence version replaced gi:5579000.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

only a small overlapping clone, as we submit sequences with

numbers given in the feature table with their source databases:

Em., EMBL; Sw., SMISSPROT; TT., TREMBL; WP., WORNIPEP; Information

on the WORNEPE database can be found at

the entire insert of clone 773A18. This sequence has been finished

according to sequence map criteria as follows. An attempt is made

to resolve all sequencing problems, such as compressions and

repeats, but not necessarily within known annotated human repeat

there is an annotation using the 'unsure' feature kay.

This sequence was generated from part of bacterial clone contigs of

human chromosome 1, constructed by the Sanger Centre Chromosome 1

This sequence was generated from part of bacterial clone

Cancer Institute by the group of Pieter de Jong, For further

details see http://www.sanger.ac.uk/Radpore.med.buffalo.edu/ VECTOR: portPREP.

Incoation/Qualifiers

Incoation/Qualifiers

Incoation/Qualifiers
                                                                               HSJ773AL8 128379 bp DNA PRI 23-NOV-1999
Human DNA sequence from clone 773A18 on chromosome lp13.2-21.1
Contains genes for RAS-PELATED PROFEIR RAP-1A (CLIKG) (KREV-1
NENDTEIN) (GTP-BINDING PROTEIN SMG-P21A) (G-22K), KCND3 (potassium voltage-gated channel, Shal-related subfamily, member 3), PROBABLE ATP-DEPRNDENT RNA HELICASE P47 HOMOLOG, ESTS, STSS, GSSS and CPG Islands, complete sequence.
                                                                                                                                                                                                                                                                                                                 HTG; C21KG; CPG ISland; G-22K; CTP_BINDING PROTEIN; KCND3; KREV-1
PROTEIN; RAPIA; RAS-RELATED PROTEIN RAPI-A; SKG-P21A.
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//clone_lib="RPCI-4"
/clone_RP4-773A18"
complement(1...98)
/gene="dJ773A18.3"
/gene="dJ773A18.3"
/note="dJ773A18.3"
complement(1...98)
/gene="dJ773A18.3"
/note="dJ773A18.3"
complement(1...98)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 128379)
Coville, G.
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/note="11 copies 2 mer tt 100% conserved"
1557, 1697
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1487. .1866
/note=match: GSS: Em:AQ518605"
1535. .1556
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/db_xref="taxon:9606"
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                                RESULT 11
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DEFINITION
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[0057] .10171
/note="Tigger3(Golem) repeat: matches 1. .111 of consensus"
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/note="LlM4 repeat: matches 4324. .4430 of consensus"
9730. .9809
/note="Alu1/FRAM repeat: matches 228. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                   7074. 4274

7074. 4274

7076-"11MB6 repeat: matches 5411. ,5607 of consensus"

7106-"11MB6 repeat: matches 5594. ,6136 of consensus"

7107-"11MB6 repeat: matches 1. ,309 of consensus"

7107-"11MB6 repeat: matches 1. ,309 of consensus"

7107-"11MB6 repeat: matches 6136. ,6175 of consensus"
                                                                                      /note="ilMC1 repeat: matches 6071. .6323 of consensus" 2237. .2539
/note="Allyr repeat: matches 4. .299 of consensus" 2540. .2597
/note="ilMC1 repeat: matches 6013. .6071 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8268. 8525

//note="LimB3 repeat: matches 5916. 6183 of consensus"

8581. 8904

/note="Wiff B repeat: matches 2. .236 of consensus"

8906. 9254

/note="LiM4 repeat: matches 4791, .5146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"wER44A repeat: matches 1. .333 of consensus" 10877. .10971 /note-"LIMEC repeat: matches 2480. .2272 of consensus" 10972. .11047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9234. .9548
/note="LlM4 repeat: matches 2658. .2976 of consensus"
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/note-"Tigger3(Golem) repeat: matches 2277. .2547 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1MEc repeat: matches 1520. .2023 of consensu
11938. .12338
/note="L2 repeat: matches 1958. .2404 of consensus".
                                                                                                                                                                                                                                                                                                                                   3414. 3702
//note="Alusx repeat: matches 13. 301 of consensus"
3855. 4028
/note="MERS8C repeat: matches 29. .84 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /100. .7429
/note="Aluxa5 repeat: matches 1. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 1148. .1537 of consensus"
                                                                                                                                                                                                                              1915. .3217
/note="AluSx repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                               3222. .3352
/note="AluSc repeat: matches 1. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5776. 5852
/Note-WAIR repeat: matches 129. .209 of consensus"
//note-WAIR repeat: matches 5. .252 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6330. 6483
foote="FRAM repeat: matches 1. .156 of consensus"
6666. 6727
/note="31 copies 2 mer aa 77% conserved"
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/note="Tigger3(Golem) repeat: matches 2970. 3028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6123. .6223
/note="MIR repeat: matches 28. .138 of consensus"
                    "U6 repeat: matches 2. .107 of consensus" .2236
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/note="U6_rept
1979.
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/note-*L2 re
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                                                                                                                                      Db 97249 ATGG 97246
                                                                                  184 ATTG 187
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//noce="match: Esrs: Em:AA837720"
//noce="match: Esrs: Em:AA837720"
//noce="match: Esrs: Em:AA77250"
//noce="match: Esrs: Em:AA772504"
//noce="match: Esrs: Em:AA772504"
//noce="match: Esrs: Em:AA772504"
//noce="match: Esrs: Em:W03890"
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//noce="match: Esr
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                                                                                                                             13333. .1383. .13834. .13834. .13835. .13835. .13835. .13835. .13835. .13835. .13835. .140 f consensus" 14240. .14335 .14652. .14652. .14652. .14652. .14652. .13801)

complement(14862. .15301)
14948. .15005
/note="match: ESTS: Em:A1673310"
15170. .15005
/note="wir repeat: matches 171. .228 of consensus"
/note="wir repeat: matches 2682. .2749 of consensus"
/note="wir repeat: matches 2682. .2749 of consensus"
/12266. .>15532
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12484. 112837
7note-"Liz repeat: matches 2029. .2370 of consensus"
7806. .1328
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// Anote="FRAM repeat: matches -2. .120 of consensus"

22908. .23214

// Anote="Allusx repeat: matches 1. .310 of consensus"

23215. .23635
                                                       12960. 13258
//note="AluSg repeat: matches 1. .299 of consensus"
13555. 13859
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Entheria; Primates; Catarrhini; Hominidae; Wertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Stone, N.E., Schmutz, J.J., Cox, D.R. and Myers, R.M.

Inpublished

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Stone, N.E., Schmutz, J.J., Cox, D.R. and Myers, R.M.

Direct Submission

Symptomic Center, B.S. Canifornia Avenue, Palo Alto, CA 94304, USA on Sep 14, 1999; this sequence version replaced 91:8822658.

NOTE: This is a "vorking draft' sequence. It currently consists of 7 contigs. The true order of the pieces arbitrary. Gaps between the contigs are represented as a strict and their order in this sequence record is a strict and Some and their order in this sequence as a soon as it is available and the accession number will be preserved.
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DNA HTG 15-SEP-1999
4, *** SEQUENCING IN PROGRESS ***, 7
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1. .200000
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                            Homo sapiens chromosome
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HTG; HTGS_PHASE1.
     AC006445 200000 bp
                                                                                                   unordered pieces.
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/organism="Homo sapiens"
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                                                     AC014817 26065 bp DNA HTG 16-NOV-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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                                                                                                                                                                                                                                                                                                                                             Adams, M. and Venter J.C.
Direct Submission
Submitted (16-Nov-1999) Celera Genomics, 45 West Gude Drive,
Submitted (16-Nov-1999) Celera Genomics, 45 West Gude Drive,
Scokrille, MD. USA
This sequence was identified as CDM:10210440 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NoTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1. 26665
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Homo sapiens clone RP11-469G4, *** SEQUENCING IN PROGRESS ***, 34
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACCGGGACTICAGIGICICCICCATCCCAGGAGCGCAGIGGCCCACIAIGGGGICIGGGCI 60
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 26065)
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Eutheria; Frimates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106791)
Waterston, R.H.
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**NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is a is not known and their order in this sequence record is a ris not known and their order in this sequence record is a ris not known and their order in this sequence record is a runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.7%; Score 33.6; DB 43; Length 26065; Best Local Similarity 59.4%; Pred. No. 2.8; Matches 57; Conservative 0; Mismatches 39; Indels 0;
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5960 c 5929 g 6855 t
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                                                                                                                                                                                                  fruit fly.
Drosophila melanogaster
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AC014817.1 GI:6436518
HTG; HTGS_PHASE2.
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Waterston, R.H.
Direct Submission
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HTG; HTGS_PHASE1.
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AVKHHUGHOKRRELLEDDOQAMERRE
SIZAHHQUPGKRELLEDDOQAMERRE
SIZAHHAQVEKLARKALRRAFTHWKHYMLLCAERAOPEMAEBHHRISOLLLHRFW
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GLEMAILIAREOLLYRSWRHHQDAAAHYGOEWOYYGAHHRIGKAKAFCLWRESAO
GLRTERTGRYRAAEFHWAOLLRWAWSQWRECLAARGAERQKLWRADLHHGHYYHYYLYH
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Nagase-T., Ishikawa,K., Miyajima,N., Tanaka,A., Kotani,H.,
Nomura,N. and Ohara,O.
The complete sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro
DNA Res. 5 (1), 31-39 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 5280)

Obara, O., Nagase, T. and Ishikawa, K.

Direct Submission
Submitted (13-FEB-1998) to the DDBJ/EMBL/GenBank databases. Osamu Ohara, Kazusa DNA Research Institute, DNA Technology; 1532-3 rana, Klazrazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
                                                                                                                                                                                                                                                                                   21073 TACCACTGTCCTCCACAAACCCTGCACATTTCCTCATTTCACTCATATAAAGGCCCAT 21014
                                                                                                                                                                                                                                                115 TATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABOIIII4.1 GI:3043607
KIAAAD542 protein.
Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII
plus clone:HG4235.
                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                               14.6%; Score 33.4; DB 45; Length 106791; 55.7%; Pred. No. 3.5; 1ve 0; Mismatches 51; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB011114 5280 bp mRNA PRI 10-
Homo sapiens mRNA for KIAA0542 protein, complete cds
AB011114
                                                   633 others
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30926 a 22362 c 21610 g 31260 t
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                                                                                                                                                                       Similarity 55.77 64; Conservative
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RTJCERVLJVQRRENYSVQNYTRQDEDCAINFAAGYLDRGCLETWFQRWWDCSRESAQO
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EGATRLLRFAASWKASRQQLQAQQOVQAAHSLHRAVRRCATLWKQKVLGRGGKPQPLA
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tive 0; Mismatches 54; Indels 0
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Search completed: March 21, 2000, 14:42:21 Job time: 3756 sec

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd

OM nucleic - nucleic search, using sw model

March 20, 2000, 18:37:52; Search time 70.18 Seconds (without alignments) 816.386 Million cell updates/sec Run on:

US-09-092-296-2 229 1 ACCGGGACTICAGIGICICC.......CCAICICCCTICAGGGACCA 229 Title: Perfect score: Sequence:

IDENTITY_NUC Scoring table: 311585 seqs, 125096042 residues searched:

N_Geneseq_36:* Database : 0 Word size : Number of hits that pass the threshold :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

•	Description	stomach c		Mouse coxsackievir	Cell-cycle regulat	Mouse coxsackievir	1 radiation	EST clone AR34. Ne	Sequence encoding			ApoE4L protease cD	ApoE4Lx2 protease	Human ApoE4 cDNA.	Human ApoE4Lx2 cDN		Human brain-specif	Human betal,6-N-ac	cDNA encoding glyc	trypsi	Bovine trypsinogen	C		Rat NMDA receptor	ADP ribosylation f	Human COL4A6 gene.	Ξ		ene.	IL-1ra	IL-1rg	prote	Protein cognate of	New TGF-beta famil	Cartilage-derived	Human bone morphog	DNA encoding human			cDNA for human MP5
SUMMARIES	£		X04326	V28846	T02964	V50430	T18696	V86365	Q05106	N60409	N50450	660690	Q69101	T18068	T18070	T06957	T66986	057953	T77045	063794	063795	V30458_1	V30459_1	020306	T05628	V10261	V19007	T49318	X21355	X03034	X02998	071243	T60587	083695	T31601	T59729	T59405	T61412	T69695	T98191
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æ	Query Match		'n	4	m.	13.3	m.		ď	ď	12.7					•		12.4	12.4	12.2	12.2	12.2	12.2	•	•	12.1		٠	٠	•	٠	•	٠	ä	ä	•	ij	11.7	ä	ä
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Query Match 95.2%; Score 218; DB 1; Length 439; Best Local Similarity 99.6%; Pred. No. 2.5e-60; Matches 229; Conservative 0; Mismatches 0; Indels

121 TITGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCT 180

181 GGAATTGCTTGAAAAG-TCTGCCTCCTCCATCTCCCTTCAGGGACCA 229

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Mouse sex comb on Mouse sex comb on Human MPS2 cDNA. M Fetroviral DNA bas Human eyal qene co Rat GlcAI-P cDNA.	ALIG	The standard; cDNA to mRNA; 439 BP. V04366; Standard; carcinome CDNA clone HP10408. Transmembrane protein; HP10408; human; stomach cancer; ds. Location/Qualifiers Location/Qualifiers Anote *cDNA comprising the coding region (minus the stop codon) is claimed (claim 3) * V05-313
V00010 V00014 T88340 V19507 V52850 V73869	ALI(o mRNA; 439 BP. ry) cDNA clone HP10 cDNA clone HP10 n/Qualifiers l an/Qualifiers l cDNA comprising the stop codon) central in the pre- duction, gene di- seful in the pre- ductive signal a sig- seful in (also claimed) se w88498) in ularive signal a seful gene in in (also claimed) secontaining su ining the vectors compositions in proteins. The inv proteins in the secreenis in and the screenis
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3065 3065 2703 210 116624 2090		94366 standard; CDNA to mRNA; 439 BP. 804356; 30-WAR-1999 (first entry) delans stomach carcinoma cDNA clone HP1040 fluman stomach carcinoma cDNA clone fluman; stransmembrane protein; Prage a /note= cDNA comprising the stop codon; Jun-1998; Jun-14948. (WOPN-1997; Jun-14948. (WORD-1998; JUN-14948. (WORD-1998; JUN-14948. (WORD-1998; JUN-14948. (WORD-1998; JUN-14948. (WORD-1998; JUN-14948. (WORD-1999; JUN-14948. (WORD-1998; JUN-14948. (WORD-199
111.7 111.7 111.7 111.7		(first carcillator) (first carcillator) (first carcillator) (first /*t /*t // no //
######		istandard; i-1999 (file stomach can stomach can stomach can stomach can stomach can light of the
, , , , ,		i6 standa (6) standa (R-1999) 1 stomach 1 stom
.8.8.8.8.9 9.9.9.9.9 9.9.9.9.9		W08456 standard, ci y8436; 30-MAR-1999 (first Human stomach carc. Transmembrane prott Homo sapiens. Loc CDS 75; W08855508-A2. 10-DEC-1998; 03-UNN-1998; J0244, 03-UNN-1998; J0244, (FRGT -) PROTECRUR (SAGA) SAGAMI CHE KATO S. SEKINE S. WRATO S. SEKINE S. WRATO S. SEKINE S. PEDB; W88498; WRY. 99-045730/04. P-PSDB; W88498; WRY. 99-045730/04. P-PSDB; W88498; WRY. 199-045730/04. P-PSDB; W88498; APP PSDB; W88498; WRY 189-045730/04. P-PSDB; W88498; APP PSDB; W88491-5089, and the carc calls of used as an anti-pactase for gene and large-scale protein has internal transmemb sequences (see W84991-508), eukaryotic cells of used as an anti-pact scale protein has anti-pact-scale protein calls are used as anti-pact-scale protein calls are used as a religious admit large-scale protein host cells are used as anti-pact-scale protein calls are used as a religious darker seased protein calls are used as a continuous calls are used as a call calls are used as call calls are used as a call calls are used as a call calls are used as a
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us-09-092-296-2.rng

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uses).
Sequence 2923 BP;
                                                                                                                                   Similarity
                                                                                                           Query Match
Best Local S1
Matches 53;
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Key
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wew isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, lumnue diseases, inflammation or blood disorders and treatment of e.g. cancers, neurological disorders. Immune diseases, inflammation or blood disorders as Claim 1; Page 180-182; 380pp; English.

This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion protein by linking to the gene to a human immunoglobulin Fc portion (e.g. x04030) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 86 novel genes and their fragments (nucleic acid sequences: X04311-X04410; amino acid sequences W78125) which are useful for preventing, treating or ameliorating medical conditions can be compared by determining the amount of the new polypeptides: no sample or by determining the presence of mutations in the new polynucleotides.

Specific uses are described for each of the 85 polynucleotides, based on
                                                                                                                                                           Human secreted protein gene 16 clone HSHBQ68.

Human secreted protein gene 16 clone HSHBQ68.

Human secreted protein; fusion protein; gene therapy; protein therapy;
dulagnosis; tissue: cancer; tumour; neurodegenerative disorder; leukacmia;
developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW,
Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P,
209 GGAATIGCITGAAAAGCICTGCCCCCCCCCTCCCTTCAGGACCA 258
                                                                                                                        X04326 standard; DNA; 2923 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1997; US-060834.
02-OCT-1997; US-060841.
02-OCT-1997; US-060844.
02-OCT-1997; US-060865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-049547.
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12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-1997;
12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                           -DEC-1998
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DNA encoding coxsackie virus and adenovirus receptor - useful for modulation of e.g. cardiac, pancreatic or gastrointestinal infection DNA encoding coxsackie virus and adenovirus and elements sequence encodes mouse coxsackievirus and adenovirus creceptor (CAR). The present invention also describes: (1) a method for codulating CAR expression comprising contexting the call with an agent which modulates CAR protein activity or CAR nucleic acid expression, concluding the presence of CAR in a biological sample comprising contacting a biological sample with an agent comprising contacting a biological sample with an agent capable of detecting CAR protein or mans such that the presence of CAR is detected. Comprising contacting a biological sample with an agent capable of detecting CAR protein or mans such that the presence of CAR is detected. Comprising contacting a biological sample with an agent capable of certification of CAR is useful for treatment of cardiac infection of the contral nervous system, e.g. a non-specific febrill illness or infection of central nervous system, e.g. a non-specific febrille illness or infection of the respiratory or gastrointestinal tract or childhood conset diabetes mellitus. Probes derived from CAR nucleic acids are useful for hybridisation assays, and antibodies raised against CAR conset diabetes mellitus. Probes derived from CAR nucleic acids are useful for hybridisation assays, and antibodies raised against CAR include combaining CAR protein and candidate/test compound are useful sequence 1128 Bp; 297 A; 286 C; 288 G; 257 T;
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which tissues they are most highly expressed in (see X04311 for described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vacau, Vacaus (first entry)
Mouse coxsacklevirus and adenovirus receptor encoding DNA.
Mouse, coxsacklevirus, adenovirus, receptor, GAR, cardiac infection;
myocarditis, pericarditis, dilated cardiomyopathy, meningoencephalitis,
pancreatic infection; acute pancreatitis; gastrointestinal tract;
diabetes mellitus; ss.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                        14 TGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tig=_ a /*tig=_ a //*tig=_ a //*tig=_ a //*tig=_ a coxsackievirus and adenovirus receptor" //transl_except= (pos:1096, .1098.aa:Xaa) //note= "Xaa= a stop codon, the sequence is shown as continuing but gets unclear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                        Length 2923;
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                                                                                                                                                                                                                                                          31; Indels
                                                                             753 G;
                                                                                                                                                                                 Score 34.4; DB 1;
Pred. No. 0.12;
                                                                                                                                                      15.0%; Scor.
63.1%; Pred. No. v...
'-a 0; Mismatches
                                                                         818 C;
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12-SEP-1997; U16189.
13-SEP-1995; US-026100.
(DAND ) DANA FARBER CANCER INST INC.
BEGGELSON JM, Filbberg RW, HOFOWITZ MS; WPPI; 98-207384/18.
P-PSDB; W57213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1015 CICTAGATACCTICAGGCAACACA 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 CICITGACCCTCCTIGGCAGCTCA 97
                                                                     637 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V28846 standard; DNA; 1128 BP.
                                                                                                                                                                                                                                                      53; Conservative
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For preventing and treating viral infection and consackievirus B - for preventing and treating viral infection and rendering cells reuseptible to transformation by adenoviral vectors in gene therapy claim 2; Page 68-70; 88pp; English.

This cDNA molecule codes for mouse McAR protein (see W6698) that respect to and for the group B cossackieviruses (CVB). It was obtained by screening a lambda phase expression cDNA library with antiserum containing antibodies specific for mouse CVB binding protein p46, and was used to identify human HCAR CDNA (See V5042). The invention also provides host cells transformed with DNA molecules encoding activities of the scroping at the containing antibodies specific for mouse CVB binding protein p46, and was used to identify human HCAR CDNA (See V5042). The invention also provides host cells transformed with DNA molecules encoding HCAR or MCAR and methods of producing the recombinant proteins or their derivatives. These proteins, their extreaclular domains, as well as oligopeptides (See CMCAR proteins or their fragments or variants are used to prevent or treat virus infections. Expressing the DNA in cells which lack these viral receptors renders the cells susceptible to treat virus infections remains an encode or gene there were the colls which lack the recombination by adenoviral vectors carrying genes for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New gene encoding a radiation protecting checkpoint protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 AGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCCTCCTTTGACCCTCCTT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "base n at position 3648 is not identified
in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%; Score 30.4; DB 1; Length 1301; 61.2%; Pred. No. 1.6; 11ve 0; Mismatches 31; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 G;
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11-CCT-1995; U12445.
11-CCT-1994; IL-111238.
(SHOS/) SHOSHAN H Z.
(UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 C;
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T18696;
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31077. .3510
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/label= cDNA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ||| || || || || || || || || || 928 TICIGCIGICACAGGAAACG 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 GGCAGCTCACATGGAACAGG 108
                                                                                                                       (UYNY ) UNIV NEW YORK STAIE. Philipson L, Tomko RP; WPI; 98-437397/37. P-PSDB; W69698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag- b
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Best Local Similarity 61.29
Matches 49; Conservative
                                06-AUG-1998.
30-JAN-1998; U01724.
30-JAN-1997; US-036986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1301 BP;
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WPI; 96-221643/22.
P-PSDB; R94906.
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                                                                                                                                                                                                                                                                                                                   T02964 standard; cDNA; 580 BP.
T02964, 10. WAR-1996 (first entry)
01. WAR-1996 (first entry)
cell-cycle regulatory protein p15 cDNA.
cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
CCR; gene therapy; transgenic animal; cancer; cell proliferation;
ss; ds.
Mus sp.
Iocation/qualifiers
cds
                                      35 GCAGIGGCCACTATGGGGTCTGGCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 AGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCCTCCTTTGACCCTCCTT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claim 43; page 81-82; 109pp; Engilsh.

CHAIM (102964) coding for the mouse cell-cycle requilatory (CCR) protein p15 (R85118) was isolated from an embryonal carcinomal library using a probe based on a mouse CCR p13.5 CDNA (102965). The isolated cDNA can be used: to detect mutations in CCR genes that lead to cell proliferation; to breed transgenic animals to study cellular disorders involving CCR allela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V50430 standard; cDNA; 1301 BP.
V50430:
07-DEC-1998 (first entry)
MOUSE coxsackievirus and Ad2 and Ad5 receptor (MCAR) cDNA.
MCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
Ad5 receptor; mouse; infection; vaccine; gene therapy; ds.
MNus sp.
Location/Qualifiers
CDS
157. .1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation/misexpression; and to correct CCR-deficient cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serrano M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 TCACATGGAACAGGGCCGGGTATGACTTTGCAACTG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-1994; US-227371.
25-MXY-1994; US-227371.
14-SEP-1994; US-34611.
29-NOY-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
Beach DH, Demetrick DJ, Hannon GJ, Se WHI; 95-373789/48.
P-PSDB; R85118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
91. .483
/*tag= a
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157. .1215
/*tag= a
                                                                                                                 89 GGCAGCTCACATGGAACAGG 108
                                                                                                                                                 109 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.3<sup>3</sup>
Matches 55; Conservative
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Sequence

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Gaps

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297 T;

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24-APR-1986.
17-SEP-1985; 047513.
11-JUN-1985; JP-126989.
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29-DEC-1988; US-291583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WIST-) Wistar Inst.
Linnenbach A;
WPI; 90-203091/27.
P-PSDB; R05711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                             Query Match
Best Local S
Matches 40
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This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, activity, hasmatopolesis regulating activity, tissue growth activity, hasmostatic and thrombolytic activity, chemotactic/chemokinetic activity, hasmostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity, The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tag; secreted protein; haematopolesis regulator; Islasue growth, activin; inhibin; tumour invasion auppressor; EST; human; chemotaxis; chemoXinesis; haemoStasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                              A CDNA clone (718856) codes for a novel radiation-protecting human checkpoint protein (84906), designated RAP-1, involved in regulation of cell cycle progression and/or apoptosis. It was isolated from a human CDNA ilbrary established in an immortalised xeroderma pigmentosa cell line, GM2096 (XPIMI). A CDNA (CDNA3) contg. a 46. De insert complemented UV sensitivity and was used to screen a lambda-gtl0-K562 human cDNA ilbrary. The insert represented part of the 3510 bp RAP-1 mRNA. The human checkpoint gene can be used as a marker for early detection and prevention of tumour progression or can be used to design new drugs that enhance radiotherapy or chemotherapy of diseases involving abnormal apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1831 TACCTCCTTGGACTTCTCCAAAGAAAACAAGAAAAAAGGAGGAGGATCTAGTTGGCAGCTT 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 CTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 CAGIGICICCICCAICCAGGAGCGCAGIGGCCACIAIGGGGTCIGGGCIGCCCTIGIC 70
   diagnosis and treatment of cancer and other diseases involving
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.0%; Score 29.8; DB 1; Length 3510; 51.9%; Pred. No. 3.6; tive 0; Mismatches 62; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M; WPI; 99-070076/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V86365 standard; cDNA; 291 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 51.9%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V86365,
27-APR-1999 (first entry)
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10-APR-1997; US-835913.
(GEMY ) GENETICS INST INC.
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W09845435-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 INGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTG 136
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                             115 TATGACTITGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTC 171
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human tumours
Score 29.8; DB 1; Length 291;
Pred. No. 1.5;
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                                                                                17; Indels
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Apolipoprotein-E; hyperlipidemia; arteriosclerosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor-associated antigen, GA733-2 -
Expressed in pacreatic carcinoma cells, used for tumor
immuno:therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O05106 standard; DNA; 2259 BP.
005106;
02-NOV-1990 (first entry)
Sequence encoding tumour-associated antigen GA733-1.
Pancreatic Carcinoma; GA733-1; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immuno:therapy.
Claim 2; Fig 27, 12pp; English.
Claim 2; Fig 27, 12pp; English.
peptide is produced by tumor cells, and Abs
peptide may be used in diagnosis and therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.7%; Score 29; DB 1
Best Local Similarity 52.0%; Pred. No. 5.5;
Matches 65; Conservative 0; Mismatches
                                          Pred. No. 1.5;
0; Mismatches
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307. .1275
/*tag= a
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15. .968
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                                          1 Similarity 70.29
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Claim 13, Page 43; 72pp; English.
The CDNA encodes ApoE4Lx2, a protease catalyzing the formation of the abnormal beta/A4 variant of beta-amyloid protein, which is used to develop an inhibitor for the diagnosis and teatment of Alzheimer disease. Downs syndrome, Parkinson disease, schizophrenia, hyperlipoproteinemia or cardiovascular disease. Sequence 936 BP; 149 A; 317 C; 336 G; 134 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 GAGCGCGCCTCAGCGCCATCCGCGAGCGCCTGGGGCCCCTGGTGGAACAGGGCCGCGTG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 GACTICAGIGICICCICCAICCAGGAGCGCAGIGGCCACIAIGGGGICIGGGCIGCCCC 65
                                                                                                                                                                                                                            New proteinase esterase-like proteins - used to develop prods. for the diagnosis and treatment of Alzheimer's disease and related diseases and treatment of Alzheimer's disease and related diseases as 139; 72pp; English.

The cDNA encodes Apod4L, a protease catalyzing the formation of the abnormal beta/A4 valant of beta-amyloid protein, which is used to develop an inhibitor for the diagnosis and teatment of Alzheimer disease, bowns syndrome, Parkinson diseases, schizophrenia, hyperlipoproteinemia or cardiovascular disease.

Sequence 597 BP; 64 A; 240 C; 197 G; 96 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New proteinase esterase-like proteins · used to develop prods. for the diagnosis and treatment of Alzheimer's disease and related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 12.7%; Score 29; DB 1; Length 597; Best Local Similarity 54.1%; Pred. No. 3.4; Matches 59; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ApoE4Lx2 protease cDNA.
ApoE4Lx2; protease; enzyme; Alzhelmer disease; diagnostic; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 CGGCCGCCACTGIGGCTCCCTGGCCGGCCACCGCTACAGGAGCGGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 TIGICCICCICITGACCCICCITGGCAGCICACAIGGAACAGGGCCGGG 114
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/label= ApoE4Lx2 protease
                                        /*tag= a
/label= ApoE4L protease
       Location/Qualifiers
1. .595
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ID Q69101 standard; cDNA; 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BERG/) BERGHANN J E. (PRED/) PREDDIE R E. Bergmann JE, Preddie RE; WPI; 94-234212/28.
                                                                                                                                                                                   Bergmann JE, Preddle RE; WPI; 94-234212/28.
                                                                                                  16-DEC-1993; E03581.
16-DEC-1992; CA-085924.
04-MAR-1993; US-291401.
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16-DEC-1992; CA-085924.
04-MAR-1993; US-291401.
                                                                                                                                                   (BERG/) BERGMANN J E. (PRED/) PREDDIE R E.
                                                                                                                                                                                                                   P-PSDB; R59841
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Key
cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protease; enzyme; Alzheimer disease; diagnostic; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in the
                                                                                                                                                                                                                                                                           579 GAGCGCGCCTCAGCGCCATCCGCGAGCGCCTGGGCCCCTGGTGGAACAGGGCCGCGTG 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA sequence coding for human apolipoprotein-E - and expression vectors and transformed cells contg. it Disclosure; Fig 2; 45pp; English.

The encoded protein is used to treat subjects who are deficient in apolipoprotein-E (or who produce abnormal forms of this molecule) and therefore are likely to suffer from hyperlipidemia, resulting in arteriosclerosis. It can also be used to raise antisera for detecting the protein deficiency or production of abnormal forms. Sequence 1110 BP; 198 A; 354 C; 415 G; 143 T;
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                             6 GACTICAGIGICICCICCAICCCAGGAGGGCACAGIGGCCACIAIGGGGICIGGGCIGCCC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA fragment - contg. DNA which codes human apolipoprotein E for treatment of hyperlipaemia.

Claim 3; Page 484; 8pp; Japanese.

The sequence may be used to produce the apolipoprotein E, useful treatment of hyperlipaemia.

Sequence 1110 BP; 198 A; 355 C; 414 G; 143 T;
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                                                                                                                                                                                12.7%; Score 29; DB 1; Length 1110; llarity 54.1%; pred. No. 4.3; Conservative 0; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                             66 TIGICCICCTCTIGACCCICCTTGGCAGCTCACAIGGAACAGGGCCGGG 114
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Pred. No. 4.3;
0; Mismatches 50; Indels
                                                                                                                                                                                                               50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JAN-1992 (first entry)
Sequence encoding human apolioprotein
Hyperlipaemia; ds.
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15. .968
/*tag= a
69. .965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-1983; JP-224980.
(MITU ) MITSUBISHI CHEM IND KK.
WPI; 85-188003/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                          N50450 standard; DNA; 1110 BP. N50450;
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069099;
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pes 59; Conservative
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ApoE4L; protease; enzy
Homo sapiens.
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29-NOV-1983; 224980.
29-NOV-1983; JP-2245
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 59; Conserv
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N50450
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149 A;
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                                                                                                                                                                                                                                                                                                           (PRED/) PREDDIE R E.
Bergmann JE, Preddie RE;
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Matches 59; Conservative
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27-JUN-1994; 126787.
27-JUN-1994; CA-126787.
Human ApoE4Lx2 cDNA.
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WPI; 96-151776/16.
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                                                                   Gaps
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                                                                                                           6 GACITCAGIGICICCICCAICCCAGGAGCGCAGIGGCCACIAIGGGGICIGGGCIGCCC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins and nucleic acids associated with Alzheimer's diaease used to develop products for diagnosis of Alzheimer's disease and related conditions, hyperlipoproteinaemia or cardiovascular disease
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2 Open reading frames (T18068 and T18069) identified in the appliance of the protein a post, (18211) and appliance of the proteins appead, (R92113) and appliance of the proteins are transcribed from an upstream regulatory region (T1804).

Appliance of these and of which causes Ed. and Ed. to combine to form a hybrid ORF, Appliance of these and other aequences (ase also T1805-77) in the actiology of Alzheimer's diseases (AD) provides means for inagencially Ab and related diseases, for the design of therapeutic reagents (e.g. ribozymes or antibodies) and potentially for gene
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Pred. No. 3.4;
0; Mismatches 50; Indels
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                   Score 29; DB 1; Length 936;
Pred. No. 4;
0; Mismatches 50; Indels
                                                                                                                                                                                             66 TIGICCICCICTIGACCCICCTIGGCAGCICAAGGAACAGGGCCGGG 114
                                                                                                                                                                                                                       245 CGGGCCGCCACTGTGGGCTCCCTGGCCGGCCACCTACAGGAGCGGG 197
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Alzheimer disease, beta-amyloid peptide precursor; APP; antisense, hyperlipoproteinaemia; cardiovascular disease; gene therapy; apolipoprotein; ApoE4; ss. Homo sapiens
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/*tag= a.
/*tag= a.
/transl_except= pos:505. .507:_aa:Ala
/transl_except= pos:553. .555:_aa:Ser
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T18070/C
ID T18070 standard; CDNA; 936 BP.
AC T18070;
DT 22-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                              118068/c
ID 118068 standard; cDNA; 597 BP
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Best Local Similarity 54.1%;
Matches 59; Conservative 0
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22-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-1994; 126787.
27-JUN-1994; CA-126787.
(PRED/) PREDDIE R E.
Bergmann JE, Preddle RE;
                                                              59; Conservative
                                        Local Similarity
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WPI; 96-151776/16.
P-PSDB; R92113.
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                       Query Match
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Matches
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Proteins and nucleic acids associated with Alzheimer's disease -
used to develop products for diagnosis of Alzheimer's disease and
trelated conditions, hyperlipoproteinaemia or cardiovascular disease
T related conditions, hyperlipoproteinaemia or cardiovascular disease
T claim 13, Fig 6A; 67p; English.
C 2 Open reading frames (718068 and 718069) identified in the
apolipoprotein E (ApoE) antisease sequence code for proteins
apoEd. (R92113) and apoEd.11 (R92114), respectively. Both ORRs
C are transcribed from an upstream requiatory region (718074).
C ApoEd comprises 2 alleles, one of Which causes Ed. and Ed.11 to
combine to form a hybrid ORF, ApoEd.x.2 (718070). Elucidation of
the significance of these and other sequences (see also 71805577)
in the actiology of Alzheimer's diseases (AD) provides means for
diagnosing AD and related diseases, for the design of therapeutic
therefore.
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Recombinati, human, apolipoprotein-E, ApoE, insect cells, larva;
Manduca sexte; Autographica celifornica nuclear polyhedrosis virus;
Maemolymph; ligid complex; biologically active; ds.
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Alzheimer disease; beta-amyloid peptide precursor; APP; antisense; hyperlipoproteinaemia; cardiovaacular disease; gene therapy; apolipoprotein; ApoE4LX2; ss.
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/transl_except= pos:505, .507:_aa:Ala
/transl_except= pos:553, .555:_aa:Ser
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04-JUN-1991; 05949.
04-JUN-1991; US-709949.
(WISC ) WISCONSIN ALUMNI RES FOUND.
ARTIE AD. BECKAGE NE, GRETCH DG, S.
WPI: 96-029812/03.
P-PSDB; R86791.
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/*tag= a
note="misc_signal"
62. .1015
/*tag= b
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Prodn. of recombinant apo:lipoprotein E in insects - by infecting Manduca sexta larvae with recombinant Autographica californica nuclear polyhedrosis baculovius vector.

Proclosure; Columns 11-14: lopp: English.

CC Recombinant human apolipoprotein-E (ApoE) (R86791) can be produced by preparing a genetic construct (contg. an ApoE-encoding sequence, e.g. T06957, and flanking regulatory sequences enabling the protein construct construct (contg. an ApoE-encoding sequence, e.g. T06957, and flanking regulatory sequences enabling the protein contger to be expressed in insect cells), which is then introduced into a Manduca sexta larva (using a recombinant Autographica californica nuclear polyhedrosis virus) and recovering the protein from the haemolymph of the larval host. The ApoE produced is in a form cufficiently complexed with lipids to be biologically active, which cannot be achieved in insect cell cultures, and can therefore be used in therpeutic applications.

Squence 1157 BP; 212 A; 370 C; 426 G; 149 T;
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Db 686 CGGCCCCCACTGCGCTCCCTGGCCGCCAGCCGCGGG 734
Search completed: March 20, 2000, 18:37:54
Job time: 8528 sec

66 TIGICCICCICITGACCCICCITGGCAGCICACAIGGAACAGGGCCGGG 114

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5-62 22-22 12 12-61 20-33 12-61 20-33 12-61 12-61 20-33 12-61 12-61 20-33 12-61 20-5

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Sequence 1 Sequence 3 Sequence 4 Sequence 2 Sequence 2

US-08 689-190-1 US-08 689-190-4 US-08 689-190-4 US-08 733-446-19 US-08 733-446-21 US-08 733-446-23 US-08 733-446-23 US-08 733-446-24 US-08 733-446-25 US-08 733-446-25 US-08 733-446-25 US-08 733-446-25

ALIGNMENTS

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Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 8, Appli
Sequence 1, Appli
                                                                                                                                        March 22, 2000, 01:22:29; Search time 50.59 Seconds (Without alignments) 541.934 Million cell updates/sec
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229
1 ACCGGGACTICAGIGICICC.......CCAICICCCTICAGGGACCA
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Copyright (c) 1993 - 1998 Compugen Ltd.
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US-08-323-465-14
US-08-323-465-14
S185254-3
US-08-69-210-8
US-08-910-90-8
US-08-494-168-1
US-08-485-449-1
PCT-US95-08493-12
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US-08-469-688-1
US-08-852-153-7
US-08-28-58-1
US-08-76-858A-4
US-09-166-203-1
US-08-375-709-1
US-08-375-709-1
US-08-375-929-1
US-08-8752-929-1
US-08-878-929-1
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                                                                                                                                                                                                                                                                                                                                                                214294 seqs, 59861208 residues
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Query
Match Length DB
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Perfect score:
Sequence:
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1831 TACCTCCTTGGACTTCTCCAAAGAAAACAAGAAAAAAGGAGGAGGATCTAGTTGGCAGCTT 1890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.0%; Score 29.8; DB 3; Length 3509; Best Local Similarity 51.9%; Pred. No. 0.91; Matches 67; Conservative 0; Mismatches 62; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         оксамІSM: Homo sapiens

CELL LINE: BONG SEABLISHED XERODERMA PIGMENTOSUM GM2096-SV3

; IMMEDIATE SOURCE:

; CLONE: RAP-1 CDNA

US-08-817-436A-1
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0.200-232-463-14
US-00-232-463-14
US-00-232-463-
                                                                                       ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch, 1.44Mb storage
                                                                                                                                                                                                                                                                              SOFTWARE: ASCLI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,436A
FILING DATE: 11-UN-197
CLASSIFICATION 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: PCT/US95/12445
FILING DATE: 11-CCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Herbert
REGISTRATION NUMBER: 25,109
REFERENCE/DOCKET NUMBER: 0744.066
TELECHONE: 202-463-700
TELEPHONE: 202-463-700
TELEFAX: 202-463-700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                  COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
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COUNTRY: USA
ZIP: 22313-0299
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D.C.
U.S.
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     쉱
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                                                                                                                                                                                                                                                              Sequence 7, Application PC/TUS9504636
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION NUMBER: PCT/US95/04636
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.3%; Score 30.4; DB 6; Length 580; Best Local Similarity 57.3%; Pred. No. 0.25; Matches 55; Conservative 0; Mismatches 41; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NESCONDER 1 STATE OF THE SECONDER 1 SEQUENCE 1. APPLICATION US/08017436A

SEQUENCE 1. APPLICATION SEQUENCE 1. SECONDER 1. SERVENT CREATED SERVENT CREATED SERVENT CREATED SERVENT CREATED SEQUENCES: 3

CORRESPONDENCE ADDRESS: 3

CORRESPONDENCE ADDRESS: 3

STREET: 900 17th Street, N.W., Suite 1000

CITY: Washington
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               95 TCACATGGAACAGGGCCGGGTATGACTTTGCAACTG 130
                                                               68 AGAAAIGGICCTICGCCGCCGTGAGATIGCIACAG 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PHIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 base pairs
TYPE: nucleic acid
STANDEDNESS: Doth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: 91..480
PCT-US95-04636-7
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PCT-US95-04636-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCCACTATGGGGTCTGGGCTGCCCTT 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.9%; Score 29.6; DB 1; Length 7218; Best Local Similarity 2.3%; Pred. No. 1.5; Matches 5; Conservative 129; Mismatches 88; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Attle, Alan D
APPLICANT: Gretch, Daniel G
APPLICANT: Gretch, Deniel G
APPLICANT: Sturley, Stephen L
APPLICANT: Beckage, Nancy E
TITLE OF INVENTION: Production of Recombinant Proteins in
TITLE OF INVENTION: Insect Larvae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 CITGAAAAGICIGCTCCTCCTCCATCTCCCTTCAGGGACCA 229
                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION HATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, SLEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: (703)836-9300
TELEFRAX: 0000103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/07709949
Patent No. 5472858
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: P.O. Box 2113
CITY: Madison
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear IMMEDIATE SOURCE:
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.07-709-949-1
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626 GAGCGCGGCCTCAGCGCCATCCGCGAGCGCCTGGGGGCCCCTGGTGGAACAGGGCCGCGTG 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT: 5185254
S185124-1.
S185124-1.
PALENT NO. 5185254
FALENT NO. 5185254
TITLE CANT: LINNERBACH, ALBAN
TITLE CANT: LINNERBACH, SENE FAMILY OF TUMOR-ASSOCIATED ANTIGENS
NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/291,583
FILING DATE: 29-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.7%; Score 29; DB 1; Length 1157; Best Local Similarity 54.1%; Pred. No. 1; Matches 59; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29; DB 7; Length 2259;
Pred. No. 1.4;
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LOCATION: 62..119
PUBLICATION INFORMATION:
AUTHORS: McLean, J W
JOURNAL: Journal of Biological Chemistry
                                                                                                                                                                  ATGRNEY/AGRAT INFORMATION:
NAME: Seay, MICholas J
REGISTRATION NUMBER: 27,386
REGISTRATION NUMBER: 9629691801
TELECOMOUNICATION INFORMATION:
TELEFRA: (608) 251-5000
TELEFRA: (608) 251-9166
INFORMATION FOR SEQ ID NO: 1:
SAQUENCE CHRRACTERISTICS:
LENGTH; 1157 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA to mRNA ANTI-CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%;
52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 62..1015
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6498-6504
1984
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NO
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
FRAGMENT TYPE: N
ORIGINAL SOURCE:
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PAPELICANT: TANGGUEH, Nacyuki
APPLICANT: TANGGUEH, Nacyuki
APPLICANT: TANGGUEH, No. 58342840mi
APPLICANT: TANGGUEH, No. 58342840mi
APPLICANT: TANGGUEH, No. 58342840mi
APPLICANT: TANGGUEH, No. 58342840mi
TITLE OF INVENTION: GENE CODING IHEREFOR AND PROCESS FOR PRODUCTION THEREOF
TITLE OF INVENTION: GENE CODING IHEREFOR AND PROCESS FOR PRODUCTION THEREOF
TITLE OF INVENTION: GENE CODING IHEREFOR AND PROCESS FOR PRODUCTION THEREOF
TITLE OF INVENTION: GENE CODING IHEREFOR AND PROCESS FOR PRODUCTION THEREOF
TITLE OF INVENTION: Washington 6 Prince Sts.
COUNTRY: Alexandria
STREET: George Mason Bldg., Washington 6 Prince Sts.
CONTRY: United States
ZIP: Z22313-1404
CONPUTER: United States
ZIP: Z2331-1404
COMPUTER: TWA PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: PATENTIA Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,990
                                                                                                    123 TGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGG 182
                                           63 CCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2095;
                                                                                                                                                                                                                                                                                                                                                                   183 AATTGCTTGAAAAGTCTGCCTCCTCCATCTCCCTTCAGGGACC 228
                                                                                                                                                                                                                                                                                                                                                                                                                            367 CCATCCACCACATTCCTTTTTTTTTTCTTCTGCCAGTGCCTTGATGTACC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28.4; DB 3;
Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION HORSE:
APPLICATION NUMBER: US 08/10,230
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: US 08/110,736
FILING DATE: 24-MG-1993
APPLICATION NUMBER: JP 4-245950
FILING DATE: 24-MG-1993
APPLICATION NUMBER: JP 5-237118
FILING DATE: 06-MG-1992
ATTORNEY/ACBNT INFORMATION:
NAME: CTANG-FEULY, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               001560-215
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; LOCATION: 156..2093
US-08-910-990-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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APPLICANT: TANGGRATION:
TILLE OF INVERTION: OS TO THE TANGEREASE
TILLE OF INVERTION: GENE CODING THEREOR AND PROCESS FOR PRODUCTION THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE BURNS: Done, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
CONRESPONDENCE ADDRESS:
ADDRESSEE PREADALE FORM:
ASTRET: VITAIL ALEANDER ENDANGE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDNE COMPATION:
ASTRET: STATE: PORPY disk
COMPUTER: ENDANGE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDNE COMPATION:
ASTRET: ANG-1993
CLASSIFICATION NUMBER: BEASE BEACH RELEASE FILLONGEN BURNS:
APPLICANTON NUMBER: US 78 (2410.7)
FILING DATE: 23-NOG-1993
APPLICANTON NUMBER: UP 5-237118
FILING DATE: 31-NOG-1993
ARTORNET/ACENT HORDAY: 001560-215
FILING DATE: 31-NOG-1993
ARTORNET/ACENT HORDAY: NUMBER: UP 5-237118
FILING DATE: 31-NOG-1993
ARTORNET/ACENT HORDAY: UP 301-NOG-1993
ARTORNET/ACENT HORDAY: NUMBER: UP 5-237118
FILING DATE: 31-NOG-1993
ARTORNET/ACENT HORDAY: UP 301-NOG-1993
ARTORNET/ACENT H
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                                                                                                                                                                                                                                    77 TIGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTG 136
Gaps
                                                                          17 CICCICCATCCCAGGAGCGCAGTGGCCACTATGGGGICTGGGCTGCCCCTTGTCCTCCTC 76
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Indels
60;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-405-230-8/c
: Sequence 8, Application US/08405230
: Patent No. 5707846
Conservative
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LOCATION: 156..2093
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US-08-405-230-8
Matches
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APPLICANT: KURODA, HISAO
APPLICANT: HOTA, MAGHIKO
APPLICANT: ITO, RAZUTOSHI
TITLE OF INVENTION: GENE EXPRESSION VECTOR USING THE GENE
TITLE OF INVENTION: EXPRESSION REGULATING REGION OF THE ADP RIBOSYLATION
TITLE OF INVENTION: FACTOR
WUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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Patent No. 5824789
CENERAL INFORMATION:
TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 12.1%; Score 27.6; DB 2; Length 3088; Local Similarity 72.0%; Pred. No. 4.8; es 36; Conservative 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 GCCACTATGGGGTCTGGGCTGCCCTTGTCCTCCTCTTGACCCTCCTTGG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 GCCAGCAGGCGCCTGGCCCCTGGCCCCCCCTTTGGCCCTTTGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: OBLON, SPIVAR, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON STATE: VIRGINIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDLUCY TYPE: FLORPY disk
MEDLUCY TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,44A
FILING DATE: 07-APR-1995
CLASSIFICATION: 800
PRIOR APPLICATION BATA:
APPLICATION NUMBER: JP HEI 6-71048
FILING DATE: 08-APR-1994
ATTORNEY/AGENI INFORMATION:
NAME: Oblon, No. 5773680man F.
REGISTRATION NUMBER: 2589-024-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION 
             3932 GGCCTGGGCGCCTCGTTCTCCATCTAGGC 3903
                                                                                                                                                                                                    US-08-418-444A-1/c; Sequence 1, Application US/08418444A, Patent No. 577368; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: VIRG
COUNTRY: US
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-418-444A-1
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US-08-485-449-1
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Best Local S:
Matches 36;
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                                                                                                                                                487 CCATIGACAACAAGAITGICCACCTICGACTCCAACITGCCAATGCGCIGCAAAIGITA 428
                                                                                                                                                                                                                                                                                            63 CCCTIGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTT 122
                                                                                                                                                                                                                              123 IGCAACTGAAGCTGAAGGAGTCTTTTCTGACAARTTCCTCCTATGAGTCCAGCTTCCTGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08494168
Fatent No. 5731302
GENERAL INFORMATION
APPLICANT: Reders, Stephen T.
APPLICANT: ADOUGHOUS: Older Collagen Deficiency
TITLE OF INVENTION: of Detecting Collagen Deficiency
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
COUNTRY: Washington, D.C.
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..4465, 4469..4876, 4880..5101)
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Pred. No. 6;
0; Mismatches 39; Indels
86; Indels
                                                                                                                                                                                                                                                                                                                                                                                            183 AATIGCITGAAAAGICTGCCTCCTCCATCTCCCTTCAGGGACC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                            367 CCATCCACCACATTCTTTCTTCTGCCAGTGCCTTGATGTACC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40397/104/BABR
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APPLICATION 1435
FILING DATE:
APPLICATION 1435
PRIOR APPLICATION BOTHS:
APPLICATION NUMBE: US 08/112,465
FILING DATE: 27-AUG-193
ATTORNEY/ACENT INFORMATION:
NAME: SAXE, Bernhard D.
RECISTRATION NUMBER: 28,665
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 CCCCTTGTCCTCTTGACCCTCCTTGGC 91
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 5102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.1%;
Best Local Similarity 56.7%;
Matches 51; Conservative (
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-08-494-168-1/c
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; LOCATION:
US-08-494-168-1
80;
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Matches
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Gaps ö

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121..2961
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                                                                                                                                                                                                                                                                                                                                                         ;
LOCATION:
PCT-US95-08493-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 CCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTTGACCCTCGTTGGCAGCTCACATG 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 11.9%; Score 27.2; DB 2; Length 2122; Best Local Similarity 51.7%; Pred. No. 5.5; Matches 62; Conservative 0; Mismatches 58; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application PC/TUS9508493
GENERAL INFORMATION:
APPLICANT: Wood. Clive
APPLICANT: Wood. Clive
TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: NA
                                                                                               ZUDURTET USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURREAT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,449
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANYOLINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 34,202
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OURPATING SYSTEM: PC-FOS-MS-POS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2122 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 194..1360
US-08-485-449-1
                   STREET: 755 Page M
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
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PCT-US95-08493-12/c
                                                                                     COUNTRY:
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RECISTATION NUMBER: 37.24
RECISTATION NUMBER: 37.24
RECISTATION NUMBER: 37.24
RECISTATION NUMBER: 37.24
RECOMMUNICATION NUMBER: 37.25
RECOMMUNICATION NUMBER
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71 CCACCATGGGGGCCTGCTTCTTCTTCTGCTCAGCCCCCTGGGCGGCCTCCTGC 130
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APPLICANT: Basquez, Nicki J.
APPLICANT: Ron, Dorit
APPLICANT: Napolitano, Eugene W.
APPLICANT: Napolitano, Euge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%; Score 27; DB 4; Length 1554; 48.4%; Pred. No. 5.6; tive 0; Mismatches 80; Indels
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ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SOFTWARE: 18-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULESHAY: 29,959
REFERENCE/DOCKET NUMBER: 22,959
TELECOMUNICATION INFORMATION:
TELECHONE: (202) 887-1500
TELEFRONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 CCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAG 196
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; Sequence 4, Application US/08665647
; Patent No. 5935803
                                                TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                      TELECOMMUNICATION INFORMATION TELEPHONE: 617 542 5070 TELEFRAX: 617 542 8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.44
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Bos taurus
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                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
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76..1551
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; LOCATION:
US-08-469-658-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 GAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCT 161
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APPLICANT: Th egersen, Hans Christian
APPLICANT: Th egersen, Hans Christian
APPLICANT: Holter, Thor Las
APPLICANT: Elector, Michael
TILLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
TILLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
SIAFE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.8%; Score 27; DB 2; Length 1554; Best Local Similarity 48.4%; Pred. No. 5.6; Matches 75; Conservative 0; Mismatches 80; Indels
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COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: FEDIULITY 4, 1994
CLASSIFICATION NUMBER: 08/192,060
FILING DATE: FEDIULITY 4, 1994
CLASSIFICATION NUMBER: 08/192,060
ATTORNEY/AGENT INFORMATION:
NUMBE: PAULI C.CLASK
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 CCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAG 196
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Patent No. 5917018
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INPCHATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: 11near
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
FEATURE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 76..1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
US-08-469-486-1
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US-08-469-658-1
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Gaps

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                                                                                                                                                                              Query Match
11.8%; Score 27; DB 4; Length 1294;
Best Local Similarity 46.5%; Pred. No. 5.1;
Matches 87; Conservative 0; Mismatches 100; Indels
TELEX: 90-4030 MESNFOERSWSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1294 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                  ) NAME/KEY: CDS
; LOCATION: 1..1293
US-08-665-647-4
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Search completed: March 22, 2000, 01:22:33 Job time: 5637 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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em_est21:*
em_est21:*
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27.0
115.3
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75.4
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35
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Copyright (c) 1993 - 1998 Compugen Ltd.
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                                                                                                                                              Title:
Perfect score:
Sequence:
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em_gss4:* gb_gss5:*

A1857998 wj69b01.x A0718761 8E.5511_B A1136523 U1-R-C2P-F06958 HSCIQCIOI N A0838514 ME_SO11_A AA37656 EST88915 AA769782 ah71b05.s

A1857998 AQ718761 A1136523 F06958 AQ838514 AA376266 AA769782

888 33 33 33 33 33 33

404 328 348 348 509 412

Description

а

DB

Length

SUMMARIES

gb_gssll:*
em_gssl2:*
gb_gssl2:*
gb_gssl3:*
gb_gssl4:*
gb_gssl4:*

em_gss10:

Seq primer: -400P from Gibco High quality sequence stop: 395. Location/Qualiflers Source // Arganism="Homo sapiens" // Clone="IMAGE:240804!" // Clone="IMAGE:240804!" // Lissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and metastatic) // Abbost="Bullo" (4 pooled tumors, including primary and metastatic) // Abbost="Bullo" (4 pooled tumors, including primary and metastatic) // Abbost="Bullo" (4 pooled tumors, including primary and metastatic) // Abbost="Bullo" (4 pooled tumors, including primary and metastatic) // Abbost="Bullo" (4 pooled tumors, including primary and metastatic) // Abbost="Bullo" (4 pooled tumors, including primary and metastatic) // Abbost="Bullo" (4 pooled tumors, including primary and modified bolylinker; ist strand conn with a Not I -011go(dT) primer. Double-stranded cDNA was ligated to Booled lung tumor tissue, and was then primed with a Not I -011go(dT) primer. Double-stranded cDNA was ligated to Booled into the Not I and Eco RI sites of the modified prill vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonado. BASE COUNT 97 a 105 c 117 g 84 t 1 others	Query Match 49.3%; Score 113; DB 61; Length 404; Best Local Similarity 98.4%; Pred. No. 2.5e-23; 1; Indels 1; Gaps 1; Matches 124; Conservative 0; Mismatches 1; Indels 1; Gaps 1; QY 105 CAGGGCGGGTATGACTTTGCAACTGAAGCTGAAGGACTTTTCTGACAATTCCTCCT 164 Db 311 CAGGGCGGGTATGACTTTGCAACTGAAGGTGAAGGTCTTTTCTGCAATTCCTCCT 252 QY 165 ATGAGTCCAGCTTCTGCAACTTGAAAAGTTCTCTCACCTCCTCCTCCTCTCCT 252 QY 224 GGACCA 229 QY 224 GGACCA 186 Db 191 GGACCA 186	RESULT 2 AQ718761/C LOCUS DEFINITION HS_551B_18_P09_27A RPCI-11 Human Male BAC Library Homo saplens accession VERSION VERSION AQ718761 AQ718761 GIS468077 AG718761 GIS548077 KETWORDS GSS SOURCE ORGANISM Homo saplens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Malalras; Catarrhini; Hominidae; Homo. THOMAINSM Homo saplens AG718761. GI:5468077 AG16r.A.; Shaker, R.; Furlong, J.; Young, J.; Zhao, S.; Adams, M.D. and Hood, L. TITLE Sequence-tagged connectors: A sequence approach to mapping and Scanning the human genome JOURNAL FOCHEACT: Malalrass GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Email: JWallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC Library availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from
C 8 34.4 15.0 458 49 AL632159 AL632159 L62612.x C 9 34.4 15.0 470 60 AL803229 AL803529 Cc22111.x C 10 32.4 14.1 537 64 AN078074 AN078074 Fc24b05.y C 11 32.4 14.1 537 24 AN078074 AN078074 Fc24b05.y C 12 32.2 14.1 742 27 278408 AN028453 FC8645 HCCDB011 n C 13 32.2 14.1 745 AL351147 AN08894 WS88009.x C 16 31.8 13.9 568 100 AQ290553 AN089994 WS88009.x C 16 31.8 13.9 568 100 AQ290553 AN089994 WS88009.x C 17 31.8 13.9 568 100 AQ290553 AN07871 Lambd C 20 31.6 13.8 43.8 AN07841 AN07871 Chr	30.6 13.4 709 61 AIB66474 30.6 13.4 457 103 A0550124 30.4 13.3 433 23 R94643 30.4 13.3 545 23 T44524 30.4 13.3 548 23 T46883 30.4 13.3 548 23 T46883 30.4 13.3 548 23 T46483 30.4 13.3 290 33 AA87480 30.4 13.3 529 37 H76456 30.4 13.3 497 37 T46451 30.4 13.3 497 37 T46451 30.4 13.3 445 87 A0768084 30.4 13.3 535 105 A0625402	ACESSION "J657998 404 bp mRNA EST 26-AUG-1999 ACESSION "J65901.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408041 3', mRNA sequence. ACESSION A1857998.1 GI:5511614 EST 26-AUG-1999 ACCESSION A1857998.1 GI:5511614 EST 26-AUG-1999 AL857998.1 GI:5511614 EST 26-AUG-1999 AL857998.1 GI:5511614 EST A1857998.1 GI:5511614 EST 26-AUG-1999 AL857998.1 GI:5511614 EST A187998.1 GI:5511614 EST 26-AUG-1999 AL857998.1 GI:5511614 EST A187998.1 GI:5511614 EST A187998.1 GI:5511614 EST CAPA LIDE AUGA Marmalia; EUCARP HOMO. EUCARP HOLE://www.ncb1.nlm.nlh.gov/ncicgap. I (Lasse Index 10404) I (Lasse Index 10404) I (1997) COMMENT On Jun 5, 1998 this sequence version replaced gi:3189004. CONMENT On Library Preparation: M. Bento Soares, Ph.D. CON Library Arrayed by: Greg Lennon, Ph.D. CON Library Arrayed by: Greg Lennon and Library Arra

us-09-092-296-2.rst

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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Lowa
University of Lowa
451 Ecketein Medical Research Building Iowa City, IA 52242, USA
Feat: 319 335 8250
Feat: 319 335 9565
Email: msoares@blue.weeg.ulowa.edu
The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult Lung library. CDNA Library Preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.wachington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 328)
Bonaldo,M.E., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                              /note-"Vector: pBACe3.6; Genomic sequence of BAC ends" 153 c 124 g 117 t 17 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 AACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UI-R-C2p-ng-e-02-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone UI-R-C2p-ng-e-02-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                          Length 552;
                                                                                                                                                                1. .552
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_cron="Plate=1087 Col=18 Row=L"
/clone="Plate=1087 Col=18 How=L"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Best Local Similarity 87.2%; Pred, No. 3.4e-12;
Matches 82; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 CTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                       Figure. 177
Class: BAC ends
High quality sequence stop: 552.
Location/Qualifiers
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Location/Qualifiers
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AI136523.1 GI:3637300
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Rattus norvegicus
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AI136523/c
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/note="Vector: pr773D-pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; The UI-R-C2p library, which is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C1 library.

UTR-C0 library. The UI-R-C0 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3- Sucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within the mixture. The subtracted library of origin of a clone within the mixture of the library of origin of a clone within UI-R-C1 clones from which 3' ESTS had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UI-R-C2p library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:
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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Boulgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Rabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE: molecular integration of the analysis of the human genome
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sapiens cDNA clone
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Butherla; Primates; Catarrhini; Hominidae; Homo
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Genexpress-Genethon
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
T=1: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 27.0%; Score 61.8; DB 42; Length 328; Best Local Similarity 69.5%; Pred. No. 2.8e-08; Matches 98; Conservative 0; Mismatches 42; Indels 1
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HSC1QC101 normalized infant brain cDNA Homo
-19c10, mRNA sequence.
F06958 1 GI:672595
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Email: genexpress@genethon.fr

Gaps

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Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryote; Primates; Catarrhin; Hominidae: Homo.

Eutheria; Primates; Catarrhin; Hominidae: Homo.

1 (bases 1 to 238)

S. Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Mhite, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Kelley, J.C., Liu, L.T., Marmaros, S.M., Marioto, Palanques, R.F., MoDonald, L.A., Nguyen, D.T., Penligrino, S.M.,

Moreno-Palanques, R.F., MoDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Morinips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., L.J.,

Bednarlk, D.D., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hunglun, J., Li, H., Metssner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Li, H., Metssner, P.S., Olsen, H.,

Fraser, C.M. and Vencer, J.C.

Initial assessment of human gene diversity and expression patterns

AL Nature 377 (6547 Suppl), 3-174 (1995)

NE 1240200
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EST88915 HSC172 cells II Homo sapiens cDNA 5' end, mRNA sequence.
AA376266.1 GI:2028809
                                                                                                                                                        /db_xnet_raxon:9606"
/db_xnet_raxon:9606"
/clone_iplate=587 Col=20 Row=G"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Genomic sequence of BAC ends"
a 127 c 106 g 153 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 CCITGICCICCICTIGACCCICCTIGGCAGCICACGAACAGGGCCGGGIAIGACTIT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 CCTCTTGCTAATATGTCTCTCCCTGGCAAGCTGCCAACCACTGGTCCTTGCTTACAGCTA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 GCAACTGAAGCTGAAGGAGTCTTTTCTGACAATTCCTCCTATGAGTCCAGCTTCCTGGA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 GCTAGTGGAGATGGCCAAGTGGTATGTGATAAAATGAGCCTCTGCTCTGAGTTCCAGGCC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCC 63
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Other ESTS: THC191210
Contact: Kerlavage, AR
Bloinformatics
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
15.3%; Score 35; DB 88; Length 509;
Best Local Similarity 47.3%; Pred. No. 2.7;
Matches 104; Conservative 0; Mismatches 116; Indels
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/organism="Homo sapiens"
Seg primer: SP6
Class: BAC ends
High quality sequence stop: 509.
Location/Qualifiers
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                                                                                                                                                                    1. .346
//organism='Homo sapiens'
//organism='Homo sapiens'
//organism='Homo sapiens'
//olone='Lib="normalized infant brain cDNA"
//clone_lib="normalized infant brain cDNA"
//es=="Female" total brain"
//dev_stage="3 months old"
//organ: brain; Vector: lafmid BA; Site_l: HindIII;
Site_2: Noti; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA: Normalization_method:
Bento Soares, Psychiatry
Bento Soares, No. S. in press*
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (hffo@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
contact and column: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                Junyar Addition (C. Genexpress_sequence_idt: ylc-lqc10 Genexpress_lbrary_idt: C. Genexpress_sequence_idt: ylc-lqc10 Insert Length: 639 Std Error: 0.00 Seq primer: (-21)M13_universsal High quality sequence stop: 150.
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 CTCTTGACCCTCCTTGGCAGCTCA 97
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Local Similarity 63.1%;
Les 53; Conservative (
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쉱 ð 셤

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ENKATYOTA MACKAZOR: Chordata; Craniata; Vertebrata; Mammalia;
ENKATYOTA MACKAZOR: Chordata; Craniata; Vertebrata; Mammalia;
ENTHARIA: Primates; Catarrhini; Hominidae; Homo.
Entheria; Primates; Catarrhini; Hominidae; Homo.
Entheria; Todases 1 to 458)

RNI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
On May 7, 1998 this sequence version replaced gi:3121420.
Contact: Robert Strausberg, Ph.D.
Trail: Robert Strausberg, Ph.D.
Trail: Robert Strausberginh, gov.
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Bluck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Grag Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consorthum/LiMI. at:
                                                                                                                                                                                                                                                                 /note-"Vector: pr773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand CDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
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t888e12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238094 3',
mRNA sequence.
A1632159
A1632159.1 GI:4683489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.4; DB 38; Length 412;
Pred. No. 3.7;
0; Mismatches 31; Indels 0
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/lab_host="bH108"
                              /clone="1321041"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
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High quality sequence stop: 439.
Location/Qualifiers
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1 Similarity 63.1%;
53; Conservative 0
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Eukaryota; Primates; Catarrhini; Hominidae; Homo.

St. 10 (bases 1 to 412)

Not CGAP http://www.ncbi.nlm.nih.gov/Acicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

On Jan 9, 1998 this sequence version replaced gi:936203.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

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Email: Robert Strausberg, Ph.D.

CONA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CON Soares, Ph.D.

CON
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699455
Fax: 3018699423
Email: arkerlav@tigr.org
For Colone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="ATCC (inhost):180944"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/cell_lhe="HSC172 (60PDL)"
/dev_stage="fetal"
/noce="organ: lung: Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
8 a 70 c 50 g 66 t 4 others
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ah71b05.s1 Soares_test1s_NHT Homo sapiens cDNA clone 1321041 3',
mRNA sequence.
AA769782
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 402.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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ö g ð g Length 470;

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AW078074.1 GI:6033226
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63.1%;
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Best Local Similarity 63.1%
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tunor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:ll34312.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergolh, gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence scop: 426.
Location/Qualifiers
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Eutheria, Primates, Catarrhini, Hominidae, Homo.
I bases 1 to 470)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 3.9;
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AI803529,1 GI:5368989
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Matches 53; Conservative
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A1803529/C
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygli; Bukaryota; Metazoa; Chordata; Euteleostel; Ostarlophysl; Cypriniformes; Cyprinoidea; Cyprinidae; Basborinae; Danlo.

Cyprinoidea; Cyprinidae; Rasborinae; Danlo.

CE 1 (bases 1 to 537)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Edylos,S., Hillier,L., Kucaba,T., Marthn,J., Beck,C., Wylle,T., Gluderwood,K., Steptoe,M., Theising,B., Allan,M., Bowers,Y., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. Harvey,N., Schurk,R., Waterston,R. and Wilson,R. Dackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. Dackson,Y., Cardenas,M., McCann,R., Mashu 19, 1998 this sequence version replaced gi:3136840.

On May 18, 1998 this sequence version replaced gi:3136840.

Other_ESTS felabos.

Contact: Stephen L. Johnson

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108, USA

Tel: 314 286 1800

Fax: 314 286 1800

Email: Zbrafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by: Matsouri Genter Clone distribution: Genome Systems, St. Louis,

Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis,

Massouri (web address: www.resgenc.com) and Research Genetics, Huntsville, Alabama (web address: www.resgenc.com) (email contact: info@resgen.com) and Research Genami (web address: www.resgen.com) (email contact: info@resgen.com) and Research Genami (web address: www.resgen.com) (email contact: info@resgen.com) and Research Genami (web address: www.resgen.com) (email contact: info@resgen.com) and Research Genami (web address: www.resgen.com) (email contact: info@resgen.com) and Research Genami (web address: mww.resgen.com) (email contact: info@resgen.com) and Research Genami (web address: mww.resgen.com) (email contact: info@resgen.com) and mand webser.
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/ Lab host-xii.-blue MRF"

/ note-"vector: pSPORTI: Site_1: NotI; Site_2: SalI; lst

/ note-"vector: pSPORTI: Site_1: NotI; Site_2: SalI; lst

strand cDNA was primed with a Not I - oligo(dTl15 primer

[5] pGANTAGTAGTAGAGGGCGCCCTTTTTTTTTTTTTT]

[5] pGANTAGTAGTAGAGGGCGGCCCTTTTTTTTTTTTTT]

[6] double-stranded CDNA was ligated to Sal I adaptors (BRL),

digested with Not I and cloned into the Not I and Sal I

sites of the pSPORTI vector (BRL). Library was constructed

by Matthew Clark (Lehrach lab: ICRF, London and Max Planck

Institut fuer Molekulare Genetik, Berlin). cDNAs for EST

analysis were selected following oligonucleotide

hybridization fingerprinting of arrayed clones from

zebrafish late somitogenesis (26 ss), adult liver or
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fe24b05.yl Zebrafish WashU MPIMG EST Danio rerio CDNA 5', mRNA
                                                                                                                                                                                                                                                  Gaps
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Seq primer: T3 ET from Amersham
High quality sequence stop: 498.
1. 537
/organism="banio rerio"
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/sex="mixed"
Score 34.4; DB 60; Length
Pred. No. 3.9;
0; Mismatches 31; Indels
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/clone="c-1db01"
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embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEMAIL: SDRAIGSHOWARTSON. WUSTL.edu
CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington Onlyersity Genome
Sequencing Center Clane distribution: Genome Systems, St. Louis,
Miscouri (web address: www.genomesystems.com) (email contact:
Info@genomesystems.com) and Research Genetics, Huttsyille, Alabama
web address: www.resgen.com) (email contact: info@seegen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW128453 523 bp mRNA EST 25-OCT-1999 fel6b05.yl 2ebrafish WashU MPIMG EST Danio rerio CDNA 5', mRNA
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                                                                                                                                                                                                                                                                                                                                            32 AGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCCTCCTTGACCCTCCTTGGC 91
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                                                                                                                                                                                                                                                              Length 537;
                                                                                                                                                                                                                                                 Score 32.4; DB 64; Length:
Pred. No. 16;
0: Mismatches 46; Indels
                                                                                                                                                                   1 others
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/db_xref="taxon:7955"
/clone_lib="zebrafish WashU MPIMG EST"
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WWW.rzpd.de)
Seq primer: 13 ET from Amersham
Seq primer: 13 ET from Amersham
High quality sequence stop: 488.
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/lab_host="XL1-blue MRF"
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AWI28453.1 GI:6116357
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Local Similarity 56.6%;
les 60; Conservative
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134 c
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L (basea 1 to 339)

Auffray, C., Behar, G., Bols, F., Bouchier, C., da Silva, C.,
Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,
Lorenzo, F., Mitchell, H., Mariage, Samson, R., Pietu, G., Pouliot, Y.,
Sebastiani, Rabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F08745 339 bp mRNA EST 20-FEB-1995 45C1D8011 normalized infant brain cDNA Homo sapiens cDNA clone c-1db01, mRNA sequence.
F08745.1 GI:672165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 AGAGIGGAAGICAITAAGGAGGCIGAGCAGACCCITITCCAICICCIGAACAICAGAGAC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Seq primer: (-21)M13_universal
High quality sequence stop: 277.
Location/Qualifiers
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Contact: Genethon
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 69; Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
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Best Local Similarity 56.6%; Pred. No. 16;
Matches 60; Conservative 0; Mismatches
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GTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCC 74
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VERSION
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                                       /stare_repe="total brain"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain: Vector: lafmid BA; Site_l: HindIII;
/note="Organ: brain: Vector: lafmid BA; Site_l: HindIII;
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/note="Organ: brain: Vector: tissue_type=total
brain: total mRNA was oligo-(dT) primed and directionally
brain: total mRNA was oligo-(dT) primed and directionally
lafmid BA vector. Clone library from B. Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press.
7 a ll6 c l00 g 64 t 2 others
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Eutheria: Primates; Catarrihii; Hominidae; Homo.

1 (bases 1 to 742)

Neri,C., Albanese,V., Lebre,A.S., Holbert,S., Saada,C.,

Bougueleret,L., Meder-Ewert,S., LeGall,I., Millasseau,P., Bul.H.,

Giudicelli,C., Massart,C., Guillou,S., Gervy,P., Poullier,E.,

Rigault,P., Weissenbach,J., Lennon,G., Chumakov,I., Dausset,J.,

Surrey of CAGCTG repeats in human conna representing new genes:

candidates for inherited neurological disorders

Hum. Mol. Genet. 5 (7), 1001-1009 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CCCACTGCGTGCTGCTGCCCCCCCCCCCTCGAAGCTTGGATGCCCCTNCACACCCCTTT 120
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/dev_stage="fetus"
/note="cDNA library of S. Meier-Ewert, Max Planck
Inst.f.Mol.Genetics, Berlin, FRG"
232 c 215 g 131 t 19 others
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On Apr 14, 1993 this sequence version replaced gi:837709.

Contact: Near C. Penel

27 Rue Juliette Dodu, 75010 Paris, France

ICRF close ID ICRES507204199.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                   Length 339;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                              Score 32.2; DB 21;
Pred. No. 15;
0; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GAICTICCCTGTGATGTCACCTGGACCCCTGCTG 154
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Best Local Similarity 58.5%;
Matches 55; Conservative
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278408
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Prinates; Catarrhini; Hominidae; Homo.

E 1 (Passe 1 to 477)

NCI-GZAP http://www.ncbi.nlm.nih.gov/ncicgap.

NTI-GZAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Iumor Gene Index

On Jan 14, 1998 this sequence version replaced gi:1797995.

On Jan 14, 1998 this sequence version replaced gi:1797995.

Contact: Robert Strausbergo, Ph.D.

Tel: (301) 496-1550

Emmel: Robert Strausbergon.h.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G. E. Consortium/Libra at:

www-bio.llnl.gov/Dbrp/image/image.html
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//Organism=Homo sapiens"
//Organism=Homo sapiens"
//Organism=Homo sapiens"
//Ob_xref="taxon:1906"
//Clone="InAGE:1947312"
//Clone="InAGE:1947312"
//Lissue_type="proled germ cell tumors"
//Lissue_type="proled germ cell tumors, and was then primed with a modified polylinker; lat strand coba a prepared from 3 pooled germ cell tumors, and was then primed with a Not I -
Oligo(d7) primer. Double-stranded coba Na Not I and Cloned into the Not I and Eco RI sites of the modified pr773
vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
78 a 150 c 174 g 78 t
                                                                                                                                                                                                                                                                                                                                                                           AI351147 477 bp mRNA EST 13-FEB-1999 qtl1g01.x1 NCI_CGAP_GC4 Homo sapiens CDNA clone IMAGE:1947312 3' similar to gb:M12529 APOLIPOPROTEIN E PRECURSOR (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GACTICAGICICCICCICCAGGAGGGCAGIGGCCACIAIGGGGICIGGGCIGCCCC 65
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198 escracrocrassearanseccossercocrosrocresses as secres and 257
                                                                            75 TCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAG 133
                                                                                                                                  Query Match
14.1%; Score 32.2; DB 45; Length 477;
Best Local Similarity 56.0%; Pred. No. 17;
Matches 61; Conservative 0; Mismatches 48; Indels 0;
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AI351147
AI351147.1 GI:4088353
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Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .360
/organism="Homo sapiens"
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/organism=
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Eltheria; Primates; Catarrhini; Hominidae; Homo.

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model Run on:

March 21, 2000, 13:39:45; Search time 479.47 Seconds (without alignments)
-1513.537 Million cell updates/sec US-09-092-296-1 239 1 GGCCACCGGGACTTCAGIGI.......CCCTTCAGGGACCAGCGICA 239 IDENTITY_NUC Title: Perfect score: Sequence: Scoring table:

821193 seqs, -1518192014 residues Gen Emb1:* Database : Searched:

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pb.bal:*

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ALIGNMENTS

RESULT 1 AB023048 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AB023048 192650 bp DNA PRI 20-NOV-1999 HONO saplens genomic DNA, chromosome 6p21.3, HLA class I region, AB023048 1 GI:5572603
AB023048.1 GI:5572603
HTG.
Homo saplens cell_line:9785K DNA, clone:53L9.
Homo saplens Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

50: gb_p13:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB ID Descriptio	10 AB023048 AB023048	0 AP000511 AP000511	AC0059	0 HSDJ144C9 AL096774	1 AC006445 AC006445	1 HSJ858B16 AL096768	4 AC016298 AC01629	1 HSJ773A18 AL049557	3 AC014817 AC014817	5 AC017080 AC017080 HOMO	4 AC016716 AC016716 Homo	5 AC016764 HOMO	OSU25430 U25430 Oryza sa	1 HS591N18 AL031594 Huma	AB011114 Homo s	2 AC010856 Homo	3 AC012294 AC01229	TNU93354 U93354	ATELLILI ATT 20	1 AC005595 AC0055	4 MITMI17 1.31623 Mitroco	0 AC008013 AC008013	3 AC009533 HOMO	4 AC013391 AC013391	AC000387 AC000387 Genom	1 AC003104 Homo	2 AP000846 Homo	3 AL133353 Homo	AC00958 - AC00958 - AC00958	3 ACULS4/8 HOMO	ALUZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZ	AC004296 Droso	ACULTON ACULTON HOMO	AC011612 Homo	4 ACUITAIL ACUITAIL	A80086 Seq	HSX99050 H.sapien	ACUU466U ACUU466U HOMO	1 HSb3G5 Z94160 Homo sa	AP000785 Homo	3 ACHOROA ACCORDA
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              principal Investigator: Hidetoshi Inoko Ph.D Phone:+81-463-93-1121, Fax:+81-463-94-8884, The sequence is submitted by Human Genome Sequencing in ALIS project of JST.
Japan Science and Technology Corporation (JST)
5-3, Yonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan For further infomation about this sequences, please visit our sequence archive Web Site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GDE:741215"
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/note="Rail312;"he location is between each flanking site
of PCR primers.
/db_xref="GDE:4573021"
/db_xref="GDE:4573021"
/standard_name="D651851"
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/standard_name="D6S952"
/note="UT5233:The location is between each flanking site
of PCR primers."
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108774. .108864
108774. .108864
/standard_name="D652088"
/note="SHGC-12985;The location is between each flanking
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/note="SHGC-3064;Ihe location is between each flanking site of PCR primers."
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47.4%; Score 113.4; DB 10; Length 200000;
Best Local Similarity 95.1%; Pred. No. 2e-25;
Matches 117; Conservative 0; Mismatches 6; Indels 0; G
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52605 a 47531 c 49366 g 50498
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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1 (sites)
Shina.T., Tamiya.G., Oka,A., Takishima,N., Yamagata,T.,
Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahram,S. and Inoko,H.,
Molecular dynamics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp HiA class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (29-Jan-1999) to the DDBJ/EMBL/GenBank databases. Takashi
Shilna, Tokal University School of Medicine, Department of
Molecular Infe Science 2; Bohseidai, Isehara, Kanagawa 259-1193,
Japan (E-mail:tshiina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,
Fax:81-463-94-8884)
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Direct Submission

Submitted (21-SEP-1999) to the DBBJ/EMBL/Genbank databases. Mika
Hirakawa. Japan Science and Technology Corporation (JST), Advanced
Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
Japan (E-mail:mika@tokyo.jst.go.jp,
URL:http://www.alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
Fax:81-3-5214-8470.

This sequence is conducted by Tokai University as a JST sequencing
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Shihna,S., Tamiya,G., Oka,A. and Inoko,H.
Homo sapiens 2,229,818bp genomic DNA of 6p21.3 HLA class I region
Published only in DataBase (1999) in press
2 (bases 1 to 200000)
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Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
section 10/20.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shiina, T. and Takishima, N.
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/note="clonal variation with 3' overlapping clone"
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/clone_lib="Research Genetics BAC Library"
3647 . 3932
/rpt_family="Alu"
complement(4999 . .5277)
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complement(21287. .21895)
/rpt_famlly="Alu"
22715. .22957
                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                     complement(6972. .7050)
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/rpt_family="Alu"
43194. .43372
/rpt_family="MER5"
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rpt_family="MER20"
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/rpt_family="Alu"
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                                                      AC005937 47323 bp DNA PRI 05-NOV-1998
ACOND Sapiens clone UWGC:370M23.002 from 6p21, complete sequence.
ACO05937.1 GI:3845393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                      Fred Hutchinson Cancer Research Center
The Clinical Research Division
Seattle, WA 98109-1024
2 (bases 1 to 47323)
5 Geraphty. D.E. and Olson, M.V.
Direct Submission
Consect Submission
Mashington, Box 352145, Seattle, WA 98195, USA
University of Washington Human Genome Center
Box 352145 Seattle, WA 98195
Context: Daniel E. Geraghty (geraghty@fhorc.org)
Overlapping Sequences:
5: UWGC:370ma3: 0.13 (Genbank Accession: AC005530)
3: UWGC:370ma3: 0.13 (Genbank Accession: AC004211)
                                                                                                                                                                                                                                                                                Large scale sequence analysis of the human MHC class I region Unpublished (1998)
                                                                                                                                                                       Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 47333)
Janer,M., Guillaudeux,T., Vu,Q., Kutyavin,T., Harter,H. and
Geraghty,D.E.
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of 682 bp in of 883 bp in

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of 744 bp in

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of 1425 bp in 1 unknown length

of 975 bp in length

length

unknown

651 bp in length known length

unknown

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gap of unknown length
: contig of 536 bp in length
gap of unknown length
: contig of 1039 bp in length
gap of unknown length
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gap of unknown length
contig of 721 bp in length
gap of unknown length
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contig of 3510 bp in length
gap of unknown
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contig of 787 bp in length
gap of unknown
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contig of 708 bp in length
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clone CITB-H1_2207Q23, *** SEQUENCING IN
                                                                                                                                                                                                                  0; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 291288)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 19
Unpublished
/note="clonal variation with 3' overlapping clone insertion of 17bp repeat" 11556 a 11489 c 12284 g 11994 t
                                                                                                                   Score 113.4; DB 11; Length 47323;
Pred. No. 1.9e-25;
0; Mismatches 6; Indels 0;
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Homo sapiens chromosome 19 clone C1
PROGRESS ***, 160 unordered pieces,
ACOO8878 C1:6165135
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DOE Joint Genome Institute.
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Best Local Similarity 95.18;
Matches 117; Conservative
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VERSION
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AUTHORS
TITLE
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unknown length of 639 bp in length unknown length of 864 bp in length unknown length

of 771 bp in length unknown length

f unknown length g of 2675 bp in length f unknown length g of 909 bp in length

of 531 bp in length unknown length of 549 bp in length

unknown

unknown length of 762 bp in length

length

unknown

g of 833 bp in length f unknown length g of 248 bp in length f unknown length

length

1350	wn length 9 bp in 1	· ~ ~	know 651	length op in l	length bp in l	ገ ቯገ	unknown lengtn of 701 bp in length	unknown length of 1112 bp in length	length bp in	unknown length of 852 bp in length	length bp in			~ ~ ~				unknown length of 748 bp in length		- C	lengt bp in		unknown length of 704 bp in length	unknown length of 700 bp in length	unknown length of 909 bp in length		unknown length of 1258 bp in length	unknown length of 983 bp in length		unknown lengtm of 729 bp in length	321	Leng p in	unknown length of 92 bp in length	p tr	⊣ Ըև-	6.4
contig	gap of		w m		gap of contig	gap of	gap or contig				gap of		gap or contig		gap or contig		gap or contig		gap or contig			gap of	gap or contig		gap or contig	gap of contig	gap of	gap or contig	gap of	H 154	1.59	15.5	555	9 5 5	9 5	gap of contig
50309:		51872:	52523:	53417:	54178:	54928:	55629:	56741:	58251:	59103:	60607:	61642:	62432:	62684:	64028:	68403:	69905:	70653:	72376:	73174:	73783:	74652:	75356:	76056:	76965:	77981:	79239:	80222:	81434:	82163:	82879:	83520:	83612:	83759:	84424:	85182:
48960	6	51029	51873	52524	53418	54179	54929	55630	56742	58252	59104	80909	61643	62433	62685	64029	58404	90669	70654	72377	73175	73784	74653	75357	76057	99692	77982	79240	80223	81435	82164	82880	83521	83613	83760	84425 .
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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Submitted (22-Nov-1999) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

Trequests: clonerequest@sanger.ac.uk

Trequests: clonerequest@sanger.ac.uk

The Nov 22, 1999 this sequence version replaced gi:6138775.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems,

such as compressions and repeats, but not necessarily within known

annotated human repeat sequence elements (e-g Alu). Where the

feature key.

feature key ambiguous, there is an annotation using the 'unsure'

feature key and the contract of the c
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Em.; EMEL; Sw.; SWISSPROY; Tr.; TREMEJ; Wp.; WORNERP; Information on the WORNERP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1

RP1-144C9 is from the library RPcI-1 constructed at the Roswell Rari-144C9 is from the library RPcI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further VECTOR: pcyPAC2.

This sequence is the entire insert of clone RP1-144C9.

Incation/Qualifiers

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Incation/Qualifiers

Incetto /Organism="Homo sapiens"
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Human DNA sequence from clone RPI-144C9 on chromosome lp34.3-36.ll,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 148943 GCTGCTCCTTCTGCCTGTCCCCATCTTTTTCATTTTATTTTTATTGAGACCGAGTCT 149002
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 77322)
Hall,R.
                                                                                                                                                                                                                                                                                                       Score 34.6; DB 42; Length 291288; Pred. No. 1.7; 0; Mismatches 75; Indels 0; 0
gap of unknown length

86189: contig of 1007 bp in length

gap of unknown length

87102: contig of 913 bp in length

gap of unknown length

87755: contig of 653 bp in length
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nilarity 51.3%;
Conservative 0
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Matches 79; Conserv
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HSDJ144C9/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC006445 200000 bp DNA HTG 15-SEP-1999 Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 7
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Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                         14.4%; Score 34.4; DB 10; Length 77322; 63.1%; Pred. No. 1.8; tive 0; Mismatches 31; Indels 0;
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Stone, N.E., Schmutz, J.J., Cox, D.R. and Myers, R.M. Direct Submission
Unpublished
                                                                                                                                                                                   /note="match: GSS: Em:AQ07331"
complement(24677, 25031)
/note="match: GSS: Em:AQ234890"
27999. .28360
/note="match: STS: Em:G14651"
29391. .29649
/note="match: STS: Em:G6203"
complement(37699, 37922)
                                                                                                                                                                                                                                                                                        ature complement(37609. .37922)
(note="match: GSS: Em:A0114724"
47849. .48201
/note="match: GSS: Em:A0553574.1"
ature 63243. .58346
/note="match: GSS: Em:A0142826"
21006 a 18901 c 18290 g 19125 t
                                                                                                                             /note="match: GSS: Em:AQ627537.1"
complement(11439. 11580)
/note="match: GSS: Em:AQ031787"
complement(24560. 25030)
                                    /close_lib="RECG-1"
complement(1710, 2227)
/note="match: GSS: Em:A035665"
complement(1780, 2227)
/note="match: GSS: Em:A0355618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 31240 crcradaraccrrcadgeaacaca 31217
/chromosome="1"
/map="p34.3-36.11"
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Matches 53; Conservative
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ORIGIN
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VERSION
KEYWORDS
SOURCE
ORGANISM
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REFERENCE
AUTHORS
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TITLE
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JOURNAL
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COMMENT

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Barlow, K.

Submitted (25-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire, Direct Submitted (25-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clone-request@sanger.ac.uk
On Jul 27, 1999 this sequence version replaced g1:5579004.
On Jul 27, 1999 this sequence version replaced g1:5579004.
On Jul 27, 1999 this sequence version replaced g1:579004.
Where differences are found these are annotated as variations.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
EMB: Sw: SWISSPROT: Tr:, TREMB: WP: WORMPEP: Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSJ858B16 36676 bp DNA 23-NOV-1999
HMMan DNA sequence from clone 858B16 on chromosome 22. Contains the KIAA0542 gene and a gene for a novel protein similar to hamster PSSC (Phosphatidylserine Decarboxylase Proenzyme, EC 4.1.1.65).
Contains ESTs, GSSs and a putative CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 36776 GACAGGGTATCACTCTGTTGCCCAAGCTAAAGTGCAGTTACATGATAATGACTCACTGTA 36835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 GGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATG 171
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 36676)
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ALO96768 GI:5596770
HTG: CpG Island; KIAA0542; Phosphatidylserine Decarboxylase
Proenzyme; PS5C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.3%; Score 34.2; DB 41; Length 200000; Best Local Similarity 57.7%; Pred. No. 2.2; Matches 60; Conservative 0; Mismatches 44; Indels 0;
1169: contig of 1169 bp in length 1568: gap of unknown length 1739: gap of unknown length 1739: gap of unknown length 1739: gap of unknown length 1737: contig of 10533 bp in length 1732: gap of unknown length 1734: gap of unknown length 17329: gap of unknown length 16880: contig of 36476 bp in length 16880: contig of 4752 bp in length 165348: gap of unknown length 1654548: gap 
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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PTASTGPELLILPLISSEMPCGAAAPARVSAQRATPRDKPPVPSSLASVPDPHLILPGD
FSATRAGPELSTAGSLDIEAELEETQQQLLHYQTTKQNIWSCRRQASSLRRMLELNRE
EPGPEDGEVEQQVQKELEQVEWQIQLLAEELQAQRQPIGACVARIQALKQALC"
1016 (<273. 454,1413. 1488,1978. 2073,2538. 2614,
3977. 4099,5606. 5702,8812. 8972,9435. 9509,10811. 10885,
11023. 11199,11271. 11528)
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/product-du858161.2 (KIAA0542 (isoform 2))"
/product-du858161.2 (isoform 2))"
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/db_xref="G1:5921490".
                                                                                                                                                                                                                                                                                                                 /note="original published form; could be artefactual as it is result of a large intron read-through; match; proteins: Tr:060289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WALQAYQQQLLQEGATRLLRFAASMKASRQQLQAQQQYQAAHSLHRAVRRCATLWKQK
VLGRGGKPQPLAAIAPSRKVTFEGPLLNRIAAGAGDGTLETKRPQASRPLGALGRLAA
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complement(join(16160. .17505,18222. .18382,18665. .18811,
19003. .19141,19318. .19554,21353. .21518,23432. .23685,
28473. .288491)
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//gene="dd858b16.2"

Em.AF0533304 Em.B2163 Em.M62722 Em.AL050371 Em.AF086277

Em.AF0233304 Em.G82112 Em.AB011114; match: ESTs:

Em.AA324939 Em.AA682112 Em.AA166445 Em.AA166440

Em.AA260704 Em.A101975 Em.AL039237 Em:AA118158

Em.RA289212 Em.A123370 Em.AU035550 Em.AA12337

Em.AA717291 Em.AA326672 Em.AU051210 Em.AA298268
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/note="Alusx repeat: matches 21. .312 of consensus" 4650. .4754

/note="Alusy x repeat: matches 200. .307 of consensus" 4990. .5281

/note="Alusx repeat: matches 1. .292 of consensus" 5806. .5231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MLTIC repeat: matches 6. .460 of consensus" 6529. .6668
/note="RAM repeat: matches 1. .140 of consensus" 6671. .6966
/note="RAM repeat: matches 1. .295 of consensus" 6985. .7081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat: matches 2497. .2701 of consensus"
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/note="112 repeat: matches 1570. .2750 of consensus. 15108. .15404
complement(16160)
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2099. .12259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620. .913
/note="AluSx repeat: matches 1. .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3250. .3536
/mote="AluJo repeat; matches 2. .302 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1444. 1687
/gene="dJ858B16.1"
/hote="match: GSS: Em:AQ545234"
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/note="MIR rej
9766. .10068
/note="Aluy ro
10069. .10096
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/note="L2 re
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3397. .4099,5606. .5702,8812. .8972,9435. .9509,10811. .10885,
11023. .11199,11271. .11524,12717. .12948,14414. .14546,
14669. .14747,12784. .15895,15983. .16217)
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join(c273. .454.4413. .1488.1978. .2073.2538 .
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3997. .4099,5606. .5702,8812. .8952,9435. .9509,10811. .10885,
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14669. .14747,15784. .15895,15983. .16087)
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// June 2000-2010.1.
// June 2000-2010.1.
// June 2010-2010.1.
// June 2010-2010.1.
// June 2010-2010.1.
// June 2010-2010.2.
// June 2
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LHHGHSVLHRALDAWTYGGRYRAAEFTHAGILERRAWSGWEBELALEGAERGLEMEN
LHHGHSVLHRALDAWTYGGRYRS ILBEVAARESGHRRCLLEGALREWERTWARYD
AKKTFOASTHTRICS KYLUGWEAVSOWAY RRQEDCA IWEAGKYLDRGCLEFWYD
RWDCS RASAGQRLOLERA VOHHHROLLEGLARWT HHLGCYRKRLLERGSTGLLA
RAZBTGFRGWRQDLAARGDSQRATYRALWFFAFSLOAKWAWLAFYLERREKKARL
WALGAYGGLLOGARROEGRAYYRALWFFAFSLOAKWAWLAFYLERREKKARL
WLGRGRYD CHAAL ARDSHYTERPELAGAGGAGQYOAGGYOAGGGGRASHECHATWRGK
VLGRGGRYD CHAAL ARDSHYTERS PLLMRIAAGAGGTLEGTRROKSRELGALGRLAA
EEPHALELPQKPQEHGLGMAQPAAPSLTRFFIABARTALVPHSPLFBALGSLGRLAA
                                                   This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
BSBB16 is from the library RRC1-5 constructed at the Roswell Park Cancer Institute by the group of pleter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entire insert of clone 85BB16. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="QAILHAERQLLYRSWFWWHQQAAARHQEQEWQTVACAHHRHGRL
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The true left end of clone 694E4 (ALO31255) is at 36572 in this
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/product="dJ858B16.1.2 (KIAA0542 (1soform 2))"
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/Product-104388Bals.1.1 (KIAA0542 (isoform 1))"
/protein.id-10485392.1"
/db_xref="G1:5921489"
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/clone="RP5-858B16"
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/gene="dJ858B16.1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: 1 to 62181)

E Birren, B., Linton.L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RPI1-555MJ7

LI (Basea I to 62181)

E Abarna, N., Deckerly, R., Dougharkly, L., Boukhgalter, B., Blaren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Deckerly, R., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferrelra, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Ferrelra, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galgan, J., Gardyna, S., Grant, C., Hagos, B., Heaford, A., Merchan, C., Goone, P., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Mheeler, J., Wu, X., Wyman, D., Ye, W.J., Lander, A. and Zody, M., Dallara, V., Mandalla, A., Talamas, J., Wyman, D., Ye, W.J., Lander, A., And Zody, M., Dallara, J., Zimmer, A. and Zody, M., Dallara, J., Wallara, J., A., And Zody, M., Dallara, J., A., And Zody, M., Dallara, J., A., And Zody, M., J., Lander, J., Wallara, J., A., And Zody, M., J., Lander, J., Wallara, J., A., And Zody, M., J., Lander, J., Wallara, J., A., And Zody, M., J., Lander, J., Wallara, J., A., And Zody, M., J., Lander, J., Wallara, J., A., And Zody, M., J., Lander, J., Wallara, J., A., And Zody, M., J., Lander, J., Wallara, J., A., And Zody, M., J., Lander, J., Wallara, J., A., And Zody, M., J., Lander, J., Wallara, J., A., And Zody, M., J., Lander, J., Wallara, J., A., An
Em: AA144920 Em: AA673371 Em: RO0603 Em: AA297077 Em: AA237290 Em: AA61572 Em: AA229754 Em: AA297076 Em: AA63609 Em: AA61572 Em: AA229754 Em: AA297076 Em: AA290706 Em: AA63608 Em: AA004871 Em: AA229759 Em: AA149582 Em: AA636285 Em: AA0031353 Em: AA52123 Em: AA044074 Em: AA361548 Em: H69648 Em: AA046738 Em: AA637284 Em: AA04674 Em: AA6046738 Em: AA66784 Em: AA6046738 Em: AA604678 Em: AA604674 Em: AA60474 Em: AA604674 Em: AA6047 Em: AA60474 Em: AA60474 Em: AA6047 Em: AA60474 Em: AA6047 Em: AA60474 Em: AA6047 Em: AA60474 Em: AA6047
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo saplens clone RPll-655M17, LOW-PASS SEQUENCE SAMPLING.
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AC016298.1 GT:6467036
HTG: HTGS_PHASE0.
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Best Local Similarity 54.9%;
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Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBM Center code: WIBM Web site: http://www.seq.wi.mlt.edu Contact: sequence_submission@genome.wi.mit.edu ....... Project Information Center project name: 14315 Center project name: 655_M_I7
                                                                                                           * NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* configs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* architrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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Direct Submission

Direct Submission

Direct Submission

Submitted (03-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire,
CBIO [SA, WE. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

On Jul 27, 1999 this sequence version replaced gi:5579000.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMEL: SW: SWISSPROT: Ir:, TREMEL: Mp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/Wormpep This sequence is
the entire insert of clone 773Al8. This sequence has been finished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSJ773A18 128379 bp DNA PRI 23-NOV-1999 HUMAN DNA sequence from clone 773A18 on chromosome 1p13.2-21.1 CONTAINS GROSSIUS GENES FOR TAS-RELATED PROTEIN RAP-1A (C21KG) (KREV-1 PROTEIN) (GTP-BINDING PROTEIN) (G-22K), KCN3 (potassium voltage-gated channel, Shal-related subfamily, member 3), PROBABLE ATP-DEPENDENT RNA HELICASE P47 HOMOLOG, ESTS, STSS, GSSS and CpG AL049557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL049557.19 GI:5596765
HTG; C21KG; CpG Island; G-22K; GIP_BINDING PROTEIN; KCND3; KREV-1
PROTEIN; RAPIA; RAS-RELAIED PROTEIN RAPI-A; SMG-P21A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 11965 ICTICITICCTITGGCCCTGGGTIGGCAGICCCTGGAAAAGGTCCTACAATCCCTIGC 12024
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 128379)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33.8; DB 44; Length 62181;
Pred. No. 2.7;
0; Mismatches 62; Indels 0;
gap of unknown length
contig of 815 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 800 bp in length
gap of unknown length
contig of 810 bp in length
gap of unknown length
contig of 791 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 787 bp in length
gap of unknown length
contig of 804 bp in length
contig of 804 bp in length
gap of unknown length
contig of 802 bp in length
gap of unknown length
contig of 814 bp in length
gap of unknown length
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contig of 814 bp in length
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Best Local Similarity 53.48;
Matches 71; Conservative
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                               51800:
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LOCUS
DEFINITION
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
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1268. .8525
note="LIMB3 repeat: matches 5916. .6183 of consensus"
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according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chri
773A18 is from the library RPCI-4 constructed at the Roswell Park Cancer Institute by the group of Pleter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /hote="dJ773a18.3 (similar to cytokeratin 18); match:
cDNAs: Em:X12876; match: proteins: Sw:P05784 Sw:P05783"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2237. .2539
**Mote="Alur repeat: matches 4. .299 of consensus"
5540. .2597
**Mote="LIMC1 repeat: matches 6013. .6071 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4316. .4840
//hote="LiMB6 repeat: matches 5594. .6136 of consensus"
4841. .5150
//hote="AlluSp repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151. .5192
note="LIMB6 repeat: matches 6136. .6175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [979. .2236
'note-"LIMC1 repeat: matches 6071. .6323 of consensus"
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Mote="LIMB6 repeat: matches 5411. .5607 of consensus"
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/note-ahluya5 repeat: matches 1. .308 of consensus"
7838. .8216
/note-"L2 repeat: matches 1148. .1537 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1414. .3702
Moote="Alusx repeat: matches 13. .301 of consensus"
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Anote="MER58C repeat: matches 29. .84 of consensus"
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hote-"AluSx repeat: matches 1. .303 of consensus"
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note="AluSc repeat: matches 1. .131 of consensus"
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note="MIR repeat: matches 76. .206 of consensus"
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note="MIR repeat: matches 28. .138 of consensus"
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note="FRAM repeat: matches 1. .156 of consensus"
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Moote-"match: GSS: Em:AQ518605"
1535. 1556
Moote-"11 copies 2 mer tt 100% conserved"
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note="31 copies 2 mer aa 77% conserved"
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                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/chromosome="1"
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/clone="RP4-773A18"
/complement(1. .988)
/gene="d3773A18"3"
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/gene="dJ773A18.3"
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/note="MIR_re
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ote-"U6 rel
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/note="MIR r
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9606...9702

//octe="LIM4 repeat: matches 4324...4430 of consensus"
n 9730..9803

//octe="AluJ/FRAM repeat: matches 228..305 of consensus"
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consensus"
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n/octe="Tigger3(Golem) repeat: matches 1..111 of consensus"
n/octe="LiME repeat: matches 2272...2658 of consensus"
n/octe="LiME repeat: matches 1..333 of consensus"
n/octe="LiME repeat: matches 1..333 of consensus"
n/octe="LiME repeat: matches 2480...2272 of consensus"
n/octe="LiME repeat: matches 2480...2272 of consensus"
10972...10971 | 10972. | 11047 | 10047 | 10072. | 11047 | 10072. | 11048 | 111047 | 10072. | 11048 | 111047 | 10072. | 11048 | 111047 | 10072. | 11048 | 111047 | 10072. | 11048 | 11408 | 11048 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 11098 | 1 //occe=match: ESTS: Em:AI281646"
19368. 1965
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20102. .20186 Anotes-11M4 repeat: matches 4791. .5146 of consensus" 9234. .9548 . .2978 of consensus" 9550. .9605 . .9605 . .9605 . .9605 . .9605 . .9605 . .9605 . .9605 . .9605 . .9605 . .9605 . .9605 . .9002 . .9002 . .9002 . .9002 complement(14862. .15301) /note="match: ESTs: Em:AI673310" 14948. .15005 15170. .15237

Gaps

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Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC017080 106791 bp DNA HTG 09-DEC-1999
Homo sapiens clone RP11-469G4, *** SEQUENCING IN PROGRESS ***, 34
unordered pieces.
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106791)
                                                                                                                                                     5 ACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCT
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Center project name: H_NEO469GO4.

Form: This is a "working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                             Length 26065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2077: contig of 2077 bp in length 2097: gap of unknown length 6117: gap of unknown length 6117: gap of unknown length 8826: contig of 2689 bp in length 11555: gap of unknown length 11555: contig of 2729 bp in length 11852: contig of 2729 bp in length 11852: contig of 2727 bp in length 11852: contig of 2727 bp in length 11852: contig of 2968 bp in length 11852: gap of unknown length 11852: contig of 2968 bp in length 11852: contig of 2968 bp in length 11852: contig of 2968 bp in length 11852: contig of 2484 bp in length 11833: contig of 2827 bp in length 22219: gap of unknown length 26219: gap of unknown length 28539: contig of 4000 bp in length 28539: contig of 4000 bp in length 28552: contig of 4000 bp in length 28552: contig of 4000 bp in length 28551: gap of unknown length 28551: gap of unknown length 28551: contig of 4000 bp in length 28571: contig of 4000 bp in length
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of 2625 bp in length
unknown length
                                 DB 43;
                                                                                             0; Mismatches 39;
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of 2625 h
                                 Score 33.6;
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                                                                     Pred. No.
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Waterston, R.H.
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HTG; HTGS_PHASE1.
                          Query Match 14.1%;
Best Local Similarity 59.4%;
Matches 57; Conservative
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AC017080/c
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      /note="LimbEc repeat: matches 1119. .1304 of consensus-
20187. .20143
/note="AluJb repeat: matches 1. .311 of consensus"
20184. .2063
/note="LimbEc repeat: matches 1304. .1454 of consensus"
20177. .20111
/note="MillJ repeat: matches 111. .516 of consensus"
20166. .2519
/note="LimbEc repeat: matches 1509. .1991 of consensus"
/note="LimbEc repeat: matches 3. .308 of consensus"
21633. .2194
/note="LimbEc repeat: matches 3. .308 of consensus"
/note="LimbEc repeat: matches 3044. .3318 of consensus"
/note="LimbEc repeat: matches 3044. .3318 of consensus"
/note="LimbEc repeat: matches 3044. .3318 of consensus"
/note="LimbEc repeat: matches -2. .120 of consensus"
/note="RAMA repeat: matches -2. .120 of consensus"
/note="RAMA repeat: matches 1. .310 of consensus"
/note="AluJa repeat: matches 1. .310 of consensus"
/note="AluJa repeat: matches 1. .310 of consensus"
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*** SEQUENCING IN PROGRESS ***, in ordered
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This sequence was identified as CDM:10210440 by the submitter.
This sequence was identified as CDM:10210440 by the submitter.
For further information on this sequence e-mail to flyecelera.com.
* NOTE: This is a "working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 26065)
Adams, M. and Venter, J.C.
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Pred. No. 3.3;
0; Mismatches 94; Indels 0;
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/db_xref="taxon:7227"
5960 c 5929 g 6855 t
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AC014817.1 GI:6436518
HTG; HTGS_PHASE2.
fruit fly.
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Matches 90; Conservative
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AC014817/c
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Waterston, R.H.
The sequence of Homo sapiens clone
Onpublished
2 (bases 1 to 211190)
Waterston, R.H.
Waterston, R.H.
Submitted (04-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                               Homo aspiena
Eukaryota Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutharyota, Pertares, Catarrhini, Hominidae, Homo.
1 (bases 1 to 211190)
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* NOTE: This is a "working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will: * be preserved.
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Homo sapiens clone RP11-31213, *** SEQUENCING IN PROGRESS ***, 31
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HTG: HTGS_PHASE1.
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L Submission

L Submission

University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

On Dec 10. 1999 this sequence version replaced gi:6524275.

Center project name: H_NH0549613.

* NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. The true order of the pleces is not known and their order in this sequence record is a roth known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence sas soon as it is available and the accession number will

* be preserved.
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Homo sapiens clone RP11-549G13, WORKING DRAFT SEQUENCE, I unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 GCTGCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GACTITGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTAIGAGTCCAGCTT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Etheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 191010)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                         14.0%; Score 33.4; DB 44; Length 211190; 50.0%; Pred. No. 3.9; Live 0; Mismatches 82; Indels 0;
127331: contig of 10354 bp in length 127349: gap of unknown length 138238: contig of 10889 bp in length 138256: gap of unknown length 151790: contig of 13534 bp in length 151808: gap of unknown length 164982: contig of 13174 bp in length 165000: gap of unknown length 184913: gap of unknown length 184913: gap of unknown length 184913: gap of unknown length 184910: contig of 26277 bp in length.
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Location/Qualiffers
11. .191010
                                                                                                                                                                                                                                                                                                                                           540 others
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                                                                                                                                                                                                                                                                                                                    /clone-"RP11-31213"
52817 a 52007 c 53208 g 52618 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                  Location/Qualifiers
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Waterston, R.H.
                                                                                                                                                                                                                                                    1. .211190
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 50.0 Matches 82; Conservative
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138257
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164983
165001
184896
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ORGANISM
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ORIGIN
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AC016764
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DEFINITION
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AUTHORS
TITLE
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AUTHORS
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KEYWORDS
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/organism="Homo sapiens"

source

FEATURES

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Direct Submission
Submitted (20-ARR-1995) Yue-ie C. Hsing, Academia Sinica, Institute
of Botany, Yien-chu-yuan Rd. Taipei, Taiwan, 11529, Republic of
China
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Srlhllltaalavatsylllidprtplsaapapaaaraqyklekpyvillssdgfrf
GYOHKAATPHIHRLIGNGTSAATGLVPIFPTLTFPNHYSIATGLYPSSHGIINNYFPD
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NGSWFERKYDALIGFTDLEDSBEVGFLTLYFEDPHQGAGVGPDDAETTBKVYRIDE
MIGRILAGLERGYFEDYNYLIVGDHGWYGTCDKRILYFLDELAPWIKLEEDWYLSHTP
MIGRILARDEDDWALDVYAKNINGGIGSGKVENGEYLEMYLKEDLESRLHYADSYRIPPII
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euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                         Db 148271 GCAGAACCTTGCTCCTCCCTGCCGACCCACTGGGAGCTGGCACACAAGCCCCAGTGGAG 148330
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Oryza sativa nucleotide pyrophosphatase precursor, mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 148331 ccassccrrccrcasasscarsrsacrcaccscrccrccaacccrsccascs 148390
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/clone="0SB4"
/dw_stage="1 to 5 days after anthesis"
/clone_lib="constructed by Y.C. Hsing et al., Academia Slinca, Institute of Botany, Talpei, Talwan, 11529, Republic of China"
                                                                                                                                                                                                                                                                                                62 GCTGCCCCTTGTCCTCCTCTTGACCCTCGCAGCTCACATGGAACAGGGCCGGGTAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                   122 GACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTT 181
                                                                                                                                                                         Length 191010;
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/protein_id="AAA67067.1"
/db_xref="GI:818849"
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/note="signal peptide to endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSING,Y.C., TSAO,C.V., Chow,T., Hsieh,J. and Chen,Z. Rice early embryogenesis gene
                                                            468 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40. .1479
/EC_number="3.6.1.9"
/note="nucleotide phosphodiesterase"
                                                                                                                                                                         ch 14.0%; Score 33.4; DB 45; Similarity 50.0%; Pred. No. 3.9; 82; Conservative 0; Mismatches 82;
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/db_xref="taxon:9606"
/clone="RP11-549G13"
46669 a 48592 c 47516 g 47765 t
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/organism="Oryza sativa"
/strain="Tainung 67"
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Hsing, Y. C.
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http://www.sanger.artist.iniumaction.com be found at http://www.sanger.artist.iniumaction.com be found at http://www.sanger.artist.iniumaction.com be found at the Roswell Park Cancer Institute by the group of Patert de Jong. For further details see http://pacpac.med.buffalo.edu/ VECTOR: pCTPAC2 IMPORTANT: This sequence is not the entire insert of clone 591N18. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone 229A8 (286030) is at 97475 in this sequence. The true right end of clone 1042K10 (AL022238) is at 34197 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .147. .1220
'note-"AluJ/FRAM repeat: matches 217. .294 of consensus"
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'note-"HERV23 repeat: matches 1184. .1573 of consensus"
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/note="LlME1 repeat: matches 5679. 5763 of consensus"
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Anote-"LIMEL repeat: matches 5465. .5691 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="AluSg/x repeat: matches 96. 293 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585. 6665
note="Flam_A repeat: matches 27. .116 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        996 .1104
/note="FLAM_C repeat: matches 1. .108 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .282 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1869. .2134
/note="AluJb repeat: matches 21. .275 of consensus"
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forte="WER3 repeat: matches 134. .209 of consensus"
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/note="Alusx repeat: matches 1. 301 of consensus"
13936. 14230
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note="AluSc repeat: matches 4. .295 of consensus"
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note-"Alisq repeat: matches 1. .290 of consensus"
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hote="AluY repeat: matches 75. .300 of consensus"
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/note="AluJo repeat: matches 12. .282 of consensus
/note="AluX repeat: matches 1. .311 of consensus"
/note="AluX repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4854. 5144
/hote="AluJb repeat: matches 1, .308 of consensus"
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/note="AluJo repeat: matches 1. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /hote="Alusx repeat: matches 1. .299 of consensus" 8457. 8776
7/note="Alux repeat: matches 1. .311 of consensus" 9/109. .9505
        Mapping Group. Further information can be found at
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/note="MER3 repeat: matches 148.
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/note-"match: GSS AQ038173"
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="q13.1-13.2"
/clone="RP4-591N18"
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requests: concerequest@sanger.ac.uk
on Jun 11, 1999 this sequence version replaced gi.4914529.
On Jun 11, 1999 this sequence version replaced gi.4914529.
Ouring sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations where differences are found these are annotated as variations are found the overlapping clone, as we submit sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
EMB: Sw:, SWISSPROT: Tr:, TREMB!
This sequence has been finished according to sequencing problems, such as compressions and repeats, but not necessarily within known amonotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
SLPEEGYKVEMKRSDKNECGGAHGYDNAFFSMRTIFIAHGPRFEGGRVVPSFENVEIY
NVIASILNLEPAPNNGSSSFPDTILLPSE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HS591N18 97580 bp DNA PRI 23-NOV-1999 HIMID DNA sequence from clone 591N18 on chromosome 22q13.1-13.2. Contains a COXGB (Cytchrome C Oxidase subunit VID (EC 1.9.3.1)) pseudogene, ESTS, GSSs and two putative CpG islands, complete
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 97580)
Steward,C.
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                                               97. .1476
//Ec_number="3.6.1.9"
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HTG; COX6B; CpG Island; Cytochrome C Oxidase.
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22379. 22534

700ce="FRAM repeat: matches -1. .162 of consensus"
23688. -24049

700ce="MLTAM repeat: matches 1. .365 of consensus"
24.00

700ce="AlurbB repeat: matches 1. .305 of consensus"
700ce="Alurb repeat: matches 1. .310 of consensus"
7527. 25536

700ce="Alurb repeat: matches 1. .310 of consensus"
75546. .25779

700ce="Alurb repeat: matches 1. .307 of consensus"
76147. 72688

700ce="Alurs repeat: matches 1. .307 of consensus"
700ce="Alurs repeat: matches 1. .307 of consensus"
700ce="Alurs repeat: matches 1. .330 of consensus"
700ce="Alurs repeat: matches 1. .33 of consensus"
700ce="Alurs repeat: matches 1. .133 of consensus"
70cce="Alurs repeat: matches 1. .133 of consensus"
                                                                                                                                                                                                                                       /noce="Alugy repeat: matches 1. .296 of consensus"
16000. .16300
/note="Alugy repeat: matches 1. .291 of consensus"
16422. .16732
/note="Aluby repeat: matches 1. .311 of consensus"
16733. .16813 repeat: matches 2667. .2746 of consensus"
/note="L2 repeat: matches 2667. .2746 of consensus"
/note="L2 repeat: matches 2667. .2746 of consensus"
/note="match: 6888 AQ377982 AQ380087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /noce="38 copies 2 mer tt 78% conserved"
/1840. 19522
/note="SVA repeat: matches 2. .954 of consensus"
1961. .20976
/note="Tandem repeat: Some base discrepancies edited.
Assembly is consistent with Restriction Digest."
                                                                                                                                                                L2 repeat: matches 2370. .2690 of consensus"
.15910
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/note="SVA repeat: matches 521. .845 of consensus" 20051. .20854. /note="SVA repeat: matches 519. .994 of consensus" complement(20855. .20945) 21493. .21658
                                                                                                                note="MIR repeat: matches 202. .261 of consensus" 15147. .15467 natches 2370. .2690 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 2. .197 of consensus" 18063. .18376 /note="Alujb repeat: matches 1. .307 of consensus" 18652. .18837
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hote-"Alusx repeat: matches 1. .297 of consensus"
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/note="Aluub repeat: matches 1. .118 of consensus"
32118. .32408
32623. .32927
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/note="Alusg repeat: matches 1. .304 of consensus"
'note="AluSg repeat: matches 1. .297 of consensus"
                                  14237. .14466
70cte-Wilk repeat: matches 11. .261 of consensus"
7759. .14785
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/evidence=not_experimental
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                         7306e="12" Tapeat: matches 2572. .2709 of consensus" 3350. .3777

7006e="AluSx repeat: matches 1. .219 of consensus" 34284. .34597

7006e="AluSx repeat: matches 1. .312 of consensus" 35052. .35370

7006e="AluSx repeat: matches 1. .309 of consensus" 35060. .3573

7006e="MINE repeat: matches 2. .230 of consensus" 35782. .35884

7006e="MINE repeat: matches 720. .790 of consensus" 3512. .35834

7006e="MINE SERIE FERE TERESTER 
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GenCore version 4.5
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March 20, 2000, 16:15:46 ; Search time 70.18 Seconds (Without alignments) 852.036 Million cell updates/sec Run on:

US-09-092-296-1 239 1 GGCCACCGGGACTTCAGTGT......CCCTTCAGGGACCAGGGTCA 239 Title: Perfect score: Sequence:

IDENTITY_NUC Scoring table:

311585 seqs, 125096042 residues Searched:

N_Geneseq_36:* Database :

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Word size :

623170 Number of hits that pass the threshold :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	The state of the s	secreted	COX SACK 16		cycle requi	Mouse coxsackievir	EST clone AR34. Ne	c	Human apolipoprote	Sequence encoding	Human betal, 6-N-ac	O	ApoE4Lx2 protease	Human ApoE4 cDNA.		apolipor	9	. ~	a	rain-sp	Bovine trypsin gen	Bovine trypsinogen	Rat NMDA receptor	Rattus norvegicus	AUP FIDOSYLATION f	Frotein Cognate of	Wht-10b gene From	Human BAIl gene N		IL-1ra BAC	brain Expre	Serine threonine k	Disease associated	Serine protease fo	New TGF-beta famil	Cartilage-derived	in bone mo	DNA encoding human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
V28846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ន្តមូន
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.

I disorders, immune diseases, inflammation or blood disorders claim 1; Page 180-182; 380pp; English.

This sequence represents a nucleic acid molecule which encodes a secreted man protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion proteins by linking to the gene to a human immunoglobulin Fc portion of e.g. vol 302) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 86 novel genes and their fragments (nucleic acid sequences: XV4311-XV4410; amino acid sequences W7815-W7825) without are useful for preventing, treating or ameliorating medical conditions can be always determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynuclectides.

Specific uses are described for each of the 86 polynuclectides, based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein game 16 clone HSHBO68.

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; disphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AlbS; cognitive disorder; schizophrenia; prostate; obesity; osteoclas; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
          P-PSDB; W78141.
New isolated human genes and the secreted polypeptides they encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-1997; US-058972.
12-SEP-1997; US-058972.
02-0CT-1997; US-060841.
02-0CT-1997; US-06084.
02-0CT-1997; US-06084.
02-0CT-1997; US-060864.
02-0CT-1997; US-06085.
03-0CT-1997; US-06085.
03-0CT-1997; US-06085.
03-0CT-1897; US-0CT-1897; US-0CT
                                                                                                                                                                                                                                                                                                                    X04326 standard; DNA; 2923 BP
                                                                                                                                                                                                                                                                                                                                                                                                                           13-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-061060.
US-049547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-049606.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 -70N - 1998; U12125 . 02 - 027 - 1997; US - 06106 13 - 70N - 1997; US - 04954 13 - 70N - 1997; US - 04955 13 - 70N - 1997; US - 04965 13 - 70N - 1997; US - 04966 13 - 70N - 1997; US - 04961 13 - 70N - 1997; US - 04961
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13-JUN-1997;
13-JUN-1997;
13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1997; [18-AUG-1997; [12-SEP-1997; [12-SEP-1997; [13-SEP-1997; [13-SEP-1997] [13-SEP-1997; [13-SEP-1997; [13-SEP-1997; [13-SEP-1997; [13-SEP-1997] [13-SEP-1997] [13-SEP-1997; [13-SEP-1997] [13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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PAR DIAGONAL CONSACK TO ALLES AND AGENOVIUS receptor - useful for modulation of e.g. cardiac, pancreatic or gastrointestinal infection PS Disclosure, Fig 14: 104pp: Engdish.

The present sequence encodes mouse coxsackievirus and adenovirus
CC compilation CAR expression comprising contexting the cell with an agent
CC such that a cell associated activity of CAR nucleic acid expression,
CC such that a cell associated activity is altered relative to a cell
CC such that a cell associated activity is altered relative to a cell
CC comprising contacting a biological sample with an agent capable of
CC detecting CAR protein or mRNA such that the presence of CAR is detected.
CC compilation of CAR is useful for treatment of cardiac infection of the
CC contrain nervous system. e.g. a non-specific febrile illness or
CC centrain nervous system. e.g. a non-specific febrile illness or
CC contrain nervous system. e.g. a non-specific febrile illness or
CC contrain nervous system. e.g. a non-specific febrile illness or
CC contrain nervous system. e.g. and antibodies raised against CAR
CN infection of the respiratory or gastrointestinal tract or childhood
CN onset diabetes mellitus. Probes derived from CAR nucleic acids are
CN include combining CAR protein assays, and antibodies raised against CR include combining for drugs which interact with CAR protein.
CN in screening for drugs which interact with CAR protein.
CN in screening for drugs which interact with CAR protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse coxsacklevirus and ademovirus receptor encoding DNA.
Mouse; coxsacklevirus; ademovirus; receptor; CAR; cardiac infection;
Mouse; coxsacklevirus; ademovirus; receptor; CAR; cardiac infection;
pancreatic infection; acute pancreatitis; gastrointestinal tract;
diabetes mellitus; ss.
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                      /product "coxsackievirus and adenovirus receptor" /product "coxsackievirus and adenovirus receptor" /transl_except "(posi1096. 1098 as:Xaa) /note "Xaa a stop codon, the sequence is shown as continuing but gets unclear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                      DB 1; Length 2923;
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707 I:
                                                                                                                                                                      31; Indels
753 G;
                                                                           14.4%; Scor.
63.1%; Pred. No. v...
... 0; Mismatches
818 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-1997; U16189.
13-SEP-1996; US-026100.
(DAND ) DANA FARBER CANCER INST INC.
Bergelson JM. Finberg RW, Horowitz MS;
WPI; 98-207384/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .1128
                                                                                                                                                                                                                                                                                                                                                                                                                               1015 CTCTAGATACCTTCAGGCAACACA 1038
                                                                                                                                                                                                                                                                                                                                                                                  78 CICIIGACCCICCIIGGCAGCICA 101
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       637 A;
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                                                                                                                                                                             53; Conservative
2923 BP;
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Matches 50; Conserv
                                                                                                      Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; W57213
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RESULT T18696

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NR P-PSDB; R88118.

The model cycle regulating proteins bind to cyclin dependent kinase real cycle regulating proteins bind to cyclin dependent kinase real cycle regulating acids, antibodies etc., used in diagnosis and related nucleic acids, antibodies etc., used in diagnosis and the relation of the protein plant colling protein plants.

Colling (19264) coding for the mouse cell-cycle regulatory (CCR) colling plants for the mouse cell-cycle regulatory (CCR) colling plants as isolated from an embryonal carcinomal library using a probe based on a mouse CCR pla.5 cDNA (192965).

Colling plants are cell proliferation; to breed transgenic confinals to study cellular disorders involving CCR allele colling colling colling disorders involving CCR allele colling co
                                                                                                         01-MAR-1996 (first entry)
Cell-cycle regulatory protein p15 cDNA.
Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;
CCR; gene therapy; transgenic animal; cancer; cell proliferation;
SS; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 GCGGIGGCCAGGCCCGCGCAACACACATGCCCTIGTCCCGGCTGIGGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 GCAGIGGCCACTAIGGGGICIGGCCIGCCCTIGICCICCTCTIGACCCICCTIGGCAGC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human receptor for adenovirus C and coxsackievirus for preventing and treating viral infection and rendering cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1998 (first entry)
Mouse coxsacklevirus and Ad2 and Ad5 receptor (MCAR) cDNA.
MCAR: coxsacklevirus receptor; CVB; adenovirus; Ad2 receptor;
Ad5 receptor; mouse; infection; vaccine; gene therapy; ds.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-WAY-1994; US-248812.
14-SEP-1994; US-306511.
29-MOY-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
Beach DH, Demetrick DJ, Hannon GJ,
WPI; 95-373798/48.
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
91. .483
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         T02964/C

ID T02964,

TO 1.9296 standard; CDNA; 580 BP AC T02964;

DE Cell-cycle regulatory protein KW Se; ds.

OS Mus Sp.

FT Key IDCATION INTERPRETED INTERPETED INTERPRETED INTERPRETED INTERPRETED INTERPRETED INTERPRETED
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30-ZAN-1998.
30-ZAN-1999; U01724.
30-ZAN-1997; US-03698.
(UYNY ) UNIV NEW YORK STATE.
PALILISSON L TOMKO RP;
WPI: 98-437297/37.
P-PSDB; W69698.
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V50430;
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33 AGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCTCCTT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New gene encoding a radiation protecting checkpoint protein - useful for diagnosis and treatment of cancer and other diseases involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "base n at position 3648 is not identified
in the specification"
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118696;
05-201-1996 (first entry)
RAP-1 radiation proteting checkpoint protein cDNA.
RAP-1; radiation protecting checkpoint protein; apoptosis; cell death; cancer; diagnosis; therapy; radiotherapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-0CT-1995; U12445.
11-0CT-1994; IL-11238.
(SHOS/) SHOSHAN H 2.
(UVRA-) UNIV RAMOT APPLIED RES 6 IND DEV LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176. 2122
/*tag= a
31077. 3510
/*tag= b
/label= cDNA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T18696 standard; cDNA; 3510 BP
                                                                                                                                                                                 93 GGCAGCTCACATGGAACAGG 112
                                                                                                                                                                                                                                      Best Local Similarity
Matches 73; Conserv
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P-PSDB; R94906.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 CTCCTCCATCCCAGGGGGGGGGGGGCTATGGGGTCTGGGCTGCCCTTGTCCTCTC 80
                                                                                                                       119 TATGACTITGCAACTGAAGCTGAAGGACTCTTTTCTGACAAATTCCTCCTATGAGTC 175
                                                                                                                                                 immuno:therapy.
Claim 2: Fig 2A; 12pp; English.
The peptide is produced by tumor cells, and Abs raised to the peptide as used in diagnosis and therapy of human tumours. Sequence 2259 BP; 460 A; 648 C; 639 G; 512 T;
                      Score 29.8; DB 1; Length 291;
Pred. No. 1.6;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.1%; Score 29; DB 1; Length 2259; Best Local Similarity 52.0%; Pred. No. 6; Matches 65; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N60409 standard; DNA; 1110 BP.
N60409;
N60409;
Human apolipoprotein-E.
Apolipoprotein-E; hyperlipidemia; arteriosclerosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor-associated antigen, GA733-2 -
Expressed in pacreatic carcinoma cells, used for tumor
                                                                                                                                                                                                                                                                                                                                                             antigen GA733-1.
                                                                                                                                                                                                                                                                                                                                                     Sequence encoding tumour associated and
Pancreatic carcinoma; GA733-1; cancer;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
15..968
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 307. .1275 /*tag= a
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17-5EP-1985; 047513.
11-UUN-1985; JP-126989.
(MITW.) MISSUBISHI CHEM IND KK.
WPI; 86-150217/24.
P-PSDB; P60507.
                                                                                                                                                                                                                                                                    Q05106 standard; DNA; 2259 BP.
Q05106;
                              12.5%;
70.2%;
                                                                                                                                                                                                                                                                                                                                      02-NOV-1990 (first entry)
                              Query Match
Best Local Similarity 70.23
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4-JUL-1990.
29-DEC-1989; 313687.
29-DEC-1988; US-291583.
(WIST-) Wister Inst.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Linnenbach A;
WPI; 90-203091/27.
P-PSDB; R05711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1240 AAGGA 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 AAGGA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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N60409
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Q05106
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ovary, plutiary, retina and colon cDNA libraries
or dayary, pretina and colon cDNA libraries
or claim 1; page 210; 633pp; English.
This sequence represents an expressed sequence tag (EST), and is a
claim 1; page 210; 633pp; English.
This sequence represents an expressed sequence tag (EST), and is a
colonucleotide of the invention. The polynucleotides of the invention are
polynucleotide EST sequences isolated from a variety of human tissue
all secreted EST sequences and proteins encoded by them are preditted to
have useful biological activities which would make them suitable for
treating, preventing or ameliorating medical conditions in humans and
animals, although no supporting data is given. Suggested activities
animals, although activity, immune stimulating or suppressing activity,
haematopolesis requiating activity, tissue growth activity,
activin/inhibin activity, chemotactic/chemokinetic activity, anti-inflammatory
activity, cacherin/tumour invasion suppressor activity, tumour inhibition
entivity. The EST sequences are also stated to be useful for gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST clone AR34.

Expressed sequence tag; secreted protein; haematopoissis regulator;
Expressed sequence tag; secreted protein; haematopoissis regulator;
Expressed sequence tag; secreted protein; human;
chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
receptor; ilgand; anti-inflammatory; tumour inhibitor; ds.
susceptible to transformation by adenoviral vectors in gene therapy Claim 2; Page 68-70; 88pp; English.

Claim 2; Page 68-70; 88pp; English.

Claim 2; Page 68-70; 88pp; English.

Cserves as a cellular receptor for adenoviruses of the serotypes 2 cand 5 (subgroup C) and for the group B coxsackleviruses (CVB). It was obtained by screening a lambda phage expression cDNA library with antiserum containing antibodies specific for mouse CVB.

Chinding protein p46, and was used to identify human HCAR CDNA (see V50429). The invention also provides host cells transformed with DNA molecules encoding HCAR or NCAR and methods of producing the recombinant proteins or their derivatives. These proteins, their extracellular domains, as well as oligopertides (see W69699-708) which bind virus, are also provided. Isolated HCAR or WGAR proteins or their fragments or variants are used to prevent or these viral receptors renders the cells susceptible to these viral receptors renders the cells susceptible to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 AGGAGCGCAGTGGCCACTATGGGGTCTGGCCTGCCCTTGTCCTCTTGACCCTCCTT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1301;
                                                                                                                                                                                                                                                                                                                                                                                         transformation by adenoviral vectors carrying genes for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                     297 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30.4; DB 1; Length 130;
Pred. No. 1.8;
0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1999; U06954.
10-APR-1997; US-835913.
(GENY ) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
Racie La, Spaulding V, Treacy M;
WPI; 99-070076/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                     322 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                     327 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V86365 standard; cDNA; 291 BP. V86365;
                                                                                                                                                                                                                                                                                                                                                                                                                                     355 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 GGCAGCTCACATGGAACAGG 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 12.7%;
1 Similarity 61.2%;
49; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1301 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
WO9845435-A2.
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Best Local S:
Matches 49
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ApoE4L protease cDNA.
ApoE4L; protease; enzyme; Alzheimer disease; diagnostic; therapeutic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 TGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 CCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACAGGAACAGGGCCGGGTATGACTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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The CDNA encodes ApoB4L, a protease catalyzing the formation of the abnormal beta/A4 variant of beta-amyloid protein, which is used to develop an inhibitor for the diagnosis and teatment of Alzheimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New beta 1,6-N-acetyl glucose aminyl transferase - useful in sugar synthesis and for identification of cancer inhibitors, also claim 2; Page 16; 30pp; English.

DNA encoding this enzyme may be introduced into cells for box encoding this enzyme may be introduced into cells for expression. The resulting enzyme may be used to introduce, homogeneously, beta(1-6) branch structures into oligosaccharides. The enzyme may also be used to secreen for specific inhibitors gequence 2095 BP; 602 A; 481 C; 492 G; 520 T;
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(BREMANN J.E.

BERGMANN J.E.

BERGMANN J.E.

BERGMANN J.E.

PREDDIE R.E.

P-PSDB: R59841.

P-PSDB: R59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 AATIGCTIGAAAANICIGCCICCICCTCCAICTCCCTICAGGGACC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 CCAICCACCACATICCTGCTTTTCTTCTGCCAGTGCCTTGATGTACC 322
                                                                                                                                                                                                                                                                                                                                                                                        Nishikawa A, Taniguchi N, Yamaguchi N;
WPI; 94-067582/09.
P-PSDB; R48975.
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/label= ApoE4L protease
                                                                       Location/Qualifiers
156. .2093
/*tag= a
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Q69099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.19
Best Local Similarity 48.29
Matches 80; Conservative
                                                                                                                                                                                               02-MAR-1994.
24-AUG-1993; 306718.
24-AUG-1993; JP-245950.
06-AUG-1993; JP-245918.
(SUNR.) SUNTORY LTD.
(TANI/) TANIGUCHT N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA-085924.
US-291401.
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16-DEC-1993; E03581.
16-DEC-1992; CA-08592
04-MAR-1993; US-29140
                 cancer diagnosis; ds
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                                               Homo sapiens
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                    셤
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List sequence may be used to produce the apolipoprotein E, useful in the treatment of hyperlipaemia.

Sequence 1110 BP; 198 A; 355 C; 414 G; 143 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA sequence coding for human apolipoprotein-E - and expression vectors and transformed cells contg. it Disclosure; Fig 2, 45pp; English.

The encoded protein is used to treat subjects who are deficient in apolipoprotein-E (or who produce abnormal forms of this molecule) and therefore are likely to suffer from hyperlipidemia, resulting in arterioscierosis. It can also be used to raise antisera for detecting the protein deficiency or production of abnormal forms. Sequence 1110 BP; 198 A; 354 C; 415 G; 143 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579 GAGCGCGCCTCAGCGCCATCCGCGAGCGCCTGGGGCCCCTGGTGGAACAGGGCCCGCTG 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 GACTICAGIGICICCICCAICCCAGGAGCGCAGIGGCCACIAIGGGGTCIGGGCIGCCCC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA fragment – contg. DNA which codes human apolipoprotein E for treatment of hyperlipaemia.
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Betal, 6-N-acetylglucosaminyl-transferase;
acetylglucosaminotransferase; enzyme; lung carcinoma; tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.1%; Score 29; DB 1; Length 1110; Best Local Similarity 54.1%; Pred. No. 4.7; Matches 59; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 TTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      639 CGGCCGCCACTGTGGGCTCCCTGGCCGGCCGCTACAGGACGGG 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JAN-1992 (first entry)
Sequence encoding human apolioprotein E.
Hyperlipaemia; ds.
                                                                                                                                                                                                                                                                                                                                                             Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
15. .968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-NOV-1983; 224980.
29-NOV-1983; JP-224980.
(MITU ) MITSUBISHI CHEM IND KK.
WPI; 85-188003/31.
P-PSDB; P51204.
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Q57953/c
ID Q57953 standard; cDNA; 2095 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NS0450 standard; DNA; 1110 BP.
NS0450;
                                                                                                                                                                                                                                                                                                                                                         12.1%;
54.1%;
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69. .965
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 54.1
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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N50450
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Proteins and nucleic acids associated with Alzheimer's disease - teated develop products for diagnosis of Alzheimer's disease and related conditions, hyperlipoproteinsemia or cardiovascular disease and related conditions, hyperlipoproteinsemia or cardiovascular disease (Claim 9; Fig 34, 67pp; English.

C. 2 Open reading frames (T18068 and T18069) identified in the apolipoprotein E (ApoE) antisease sequence code for proteins apolitoprotein E (ApoE) antisease sequence code for proteins apoELL (R92113) and apoELLI (R92114), respectively. Both ORFs care transcribed from an upstream requistory region (T18074).

ApoE4 comprises 2 alleles, one of which causes E4L and E4L1 to combine to form a hybrid ORF, ApoE4xx2 (T18070). Elucidation of the administrance of these and other sequences (see also T18065-77) in the actiology of Alzheimer'a disease (AD) provides means for diagnosing AD and related diseases, for the design of therapeutic themselves.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 GAGCGCGGCCTCAGCGCCATCCGCGAGCGCCTGGGGGCCCTGGTGGAACAGGGCCGCGTG 246
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Bergmann JE, Preddie RE;
Bergmann JE, Preddie RE;
P-FSDB; R92115.
P-FSDB; R92115.
Proteins and nucleic acids associated with Alzheimer's disease -
used to develop products for diagnosis of Alzheimer's disease and
related conditions, hyperlipoproteinaemia or cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 TIGICCICCICTIGACCCICCITGGCAGCICACAIGGAACAGGGCCGGG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 597;
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        antisense; hyperlipoproteinaemia; cardiovascular disease; gene therapy; apolipoprotein; ApoE4; ss. Homo aapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.1%; Score 29; DB 1; Length 597 Beat Local Similarity 54.1%; Pred. No. 3.8; Matches 59; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 T;
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.555:_aa:Ser
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/transl_except= pos:505.
/transl_except= pos:553.
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                                                                                                                        Location/Qualifiers
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1. .597
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/transl_except= p
/transl_except= p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 A;
                                                                                                                                                                                                                                                                                                                                                                                27-JUN-1994; 126787.
27-JUN-1994; CA-126787.
(PRED/) PREDDIE R E.
BETGMANN JE, PTEGGIE RE;
WPI; 96-151776/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-1996 (first entry)
Human ApoE4Lx2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUN-1994; 126787.
27-JUN-1994; CA-126787.
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                NAME OF THE PROPERTY OF THE PR
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The CDNA encodes ApoE4Lx2, a protease catalyzing the formation of the abnormal beta/A variant of beta-amyloid protein, which is used to devolop an inhibitor for the disquosis and teatment of Alzheimer disease, Downs syndrome, Parkinson disease, schizophrenia, hyperlipoproteinemia or cardiovascular disease.

Sequence 936 BP; 149 A; 317 C; 336 G; 134 T;
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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disease, Downs syndrome, Parkinson disease, schizophrenia, hyperlipoproteinemia or cardiovascular disease. Sequence 597 BP; 64 A; 240 C; 197 G; 96 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 TTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 CGGGCCCCACTGTGGCTCCCTGGCCGCCAGCCGCTACAGGAGCGGG 197
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ApoE4LX2 protease cDNA.
ApoE4LX2; protease; enzyme; Alzheimer disease; diagnostic;
ApoE4LX2; stortease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 TIGICCICCICTIGACCCICCTIGGCAGCICACAIGGAACAGGGCCGGG 118
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                                                                                                                                                                                        Query Match 12.1%; Score 29; DB 1; Length 597; Best Local Similarity 54.1%; Pred. No. 3.8; Matches 59; Conservative 0; Mismatches 50; Indels
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Best Local Similarity 54.1%; Pred. No. 4.4;
Matches 59; Conservative 0; Mismatches 50; Indels
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Alzheimer disease; beta-amyloid peptide precursor; APP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/label= ApoE4Lx2 protease
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1. .934
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0691011 standard; CDNA; 936 BP
AC 069101; DE 12-7AN-1995 (first entry)
DE APOELAZ2 protease CDNA.
NW APOELAZ2; Protease; enzyme; AW therapeutic; ss.
OS HGMO Sapiens. Location/Qual FT cds 1-934 1.934
FT Cds 1-02C-1992; CA-085924.
PR 04-MAR-1993; E03581.
PR 04-MAR-1993; CA-085924.
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T18068;
22-MAY-1996 (first entry)
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Claim 13; Fig 6A; 67pp; English.

2 Open reading frames (T18068 and T18069) identified in the apolitoprotein E (ApoE) antisense sequence code for proteins apoELL (R92113) and apoELL (R92114), respectively. Both ORFs are transcribed from an upstream requiatory region (T18074).

ApoEC comprises 2 allels, one of which causes ELL and ELL1 to combine to form a hybrid ORF, ApoELLS. (T18070). Elucidation of the significance of these and other sequences (see also T18065-77) in the actiology of Alzheimer's disease (AD) provides means for diagnosing AD and related diseases, for the design of therapeutic reagents (e.g. ribozymes or antibodies) and potentially for gene therapy.
                                                                                                                                                                                                                                                                                                                         Ouery Match 12.1%; Score 29; DB 1; Length 936; Best Local Similarity 54.1%; Pred. No. 4.4; Matches 59; Conservative 0; Mismatches 50; Indels
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                                                                                                                                                                                                                                                              134 T;
                                                                                                                                                                                                                                                           336 G;
                                                                                                                                                                                                                                                              317 C;
                                                                                                                                                                                                                                                           149 A;
                                                                                                                                                                                                                                                         Sequence 936 BP;
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Search completed: March 20, 2000, 18:37:52 Job time: 8526 sec

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Sequence 3 Sequence 4 Sequence 1 Sequence 2 Sequence 2

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Query Match 13.0%; Score 31; DB 3; Length 3509; Best Local Similarity 51.0%; Pred. No. 0.45; Matches 73; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08817436A
Fatent No. 582380
GENERAL INFORMATION:
TITLE OF INVENTION: Human Checkpoint Gene and Gene for TITLE OF INVENTION: Antisense RNA thereof
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Wignan, Cohen, Leitner & Myers
STREET: 900 17th Street, N.W., Suite 1000
CITY: Washington
STREET: D.C.
STREET: D.C.
STREET: D.C.
STREET: D.S.
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CELL LINE: ESTABLISHED XERODERMA PIGMENTOSUM GM2096-SV3
IMMEDIATE SOURCE:
CLONE: RAP-1 CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOTER READABLE FORM:

MEDUUTER: 20006

COMPOTER READABLE FORM:

MEDUUTER: DESKette 3.5 inch, 1.44Mb storage COMPUTER: IBM compatible COMPUTER: SACII

CORRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/817,436A

FILING DATE: 11-UN-1997

CLASSIRICATION DATA:

APPLICATION NUMBER: DCT/US95/12445

FILING DATE: 11-CCT-1995

APPLICATION NUMBER: 074.066

FILING DATE: 11-CCT-1995

ATORNEY/AGENT INFORMATION:

NAME: COhea, HEYDERT RECEMBER: 0744.066

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAI: 202-463-7010

TELEFRAI: 202-463-701
US-08-689-190-1
US-08-689-190-3
US-08-689-190-4
US-08-733-446-20
US-08-733-446-22
US-08-733-446-23
US-08-733-446-23
US-08-733-446-24
US-08-733-446-25
US-08-733-446-25
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US-08-733-446-26
US-08-733-446-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-08-817-436A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CLONE: RJ
US-08-817-436A-1
   Sequence 1, Appli
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Sequence 1, Appli
Sequence 8, Appli
Sequence 1, Appli
                                                                                                                                                                                       March 21, 2000, 23:48:36; Search time 50.59 Seconds (without alignments) 565.599 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                         US-09-092-296-1
239
1 GGCCACGGGGACTTCAGTGT.......CCCTTCAGGGACCAGGTCA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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US-08-22-465-114
US-08-627-610-7
US-08-627-610-7
US-07-70-949-1
US-08-410-990-8
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US-08-410-990-8
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US-08-418-44A-1
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US-08-466-658-1
US-08-28-508C-1
US-08-169-948B-11
US-08-166-858A-4
US-09-166-203-41
US-08-375-709-10
US-08-375-709-10
US-08-375-709-10
US-08-375-929-11
US-08-755-929-10
US-08-755-929-10
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Perfect score:
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Sequence 7, Application US/08627610
Patent No. 2919997
Patent No. 2019997
Patent No. 2019997
Patent No. 201997
Paten
132 CTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTG 191
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                                                                                                                                                                                                                                                                                                                                                                      192 CTTGAAAANTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 TCACATGGAACAGGGCCGGGTATGACTTTGCAACTG 134
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFICATION: 800
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REFERENCE/DOCKET NUMBER: CSI-(ELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-541
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: both
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US-08-627-610-7/C
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COCATION:
US-08-627-610-7
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ZIP: 021
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                                                                                              1757 GCCCAGCCTGTGACCACCGTCCCTCCATGGGAGAGACCGAGAAAGATAACATCTCTA 1816
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                        1 GGCCACCGGGACTTCAGTGTCTCCTCCACGAGCGCAGTGGCCACTATGGGGTCTG 60
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Best Local Similarity 3.1%; Pred. No. 0.98;
Matches 7; Conservative 129; Mismatches 91; Indels
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COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232.463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 14, Application US/08232463
; Patent No. 567367
; Patent No. 567367
; Patent No. 100 
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FILING DATE: 26-AGC-1991
ATORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/COCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: Foley & Lardner
1: 1800 Diagonal Road, Suite 500
Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TGACTTTGCAACTGAAGCTGAAG 143
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-232-463-14
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IMMEDIATE SOURCE
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US-08-232-463-14
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MOLECULE TYPE: CDNA to MRNA HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_signal
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LOCATION: 62..1015
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 GCGCTGCCCAGGCCCGCGTCACTGCTGCCCCCAACATGCCCTTGTCCCCGGTCTGTGGC 69
PCT-US95-04636-7/C

Sequence 7, Application PC/TUS9504636

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 10
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ABCILICATION DATA:
CHRENT APPLICATION NUMBER: PCT/US95/04636

TTTM: NAME.
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APPLICANT: Attic, Alan D
APPLICANT: Gretch, Daniel G
APPLICANT: Sturley, Stephen L
APPLICANT: Sturley, Stephen L
APPLICANT: Brokage, Nancy E
TITLE OF INVENTION: Insect Larvae
NUMBER OF SOUGHENCES. 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: P.O. Box 2113
CITY: Madison
STATE: W1
COUNTRY: USA
ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.7%; Score 30.4; DB 6; Length 580; Best Local Similarity 57.3%; Pred. No. 0.31; Matches 55; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 TCACATGGAACAGGGCCGGGTATGACTTTGCAACTG 134
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                                                                                                                                                                                                                                                                               PETLING DATE:
CLASSIFICATION:
PRIOR PAPELGATION DATA:
PRIOR PAPELGATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR PAPELGATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-NAY-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ 10 NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: S80 base pairs
IYPE: NUCLEIC acid
STRANDENESS: Doch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07709949
Patent No. 5472858
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : LOCATION:
PCT-US95-04636-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ULT 5
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RESULT 6
US-08-405-230-8/c
Sequence 8, Application US/08405230
Patent No. 5707846
GENERAL INFORMATION:
APPLICANT: TANGGUEH, Nacyuki
APPLICANT: TANGGUEH, No. 5707846cmi
TITLE OF INVENTION: NOVEL N-ACETYLGLUCCSAMINYL TRANSFERASE
TITLE OF INVENTION: GENE CODING THEREFOR AND PROCESS FOR PRODUCTION THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bidg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.1%; Score 29; OB 1; Length 1157; Best Local Similarity 54.1%; Pred. No. 1.3; Matches 59; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 TIGICCICCICITIGACCCICCTIGGCAGCICACAIGGAACAGGGCCGGG 118
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMR FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/709,949
FILING DATE: 19910604
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: SSAY, NICHOLAS J. 7386
REFERENCE/DOCKET NUMBER: 9629691801
FELENGHUNICATION INFORMATION:
TELECHUNICATION INFORMATION:
TELECHUNICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS: McLean, J W JOURNAL: Journal of Biological Chemistry
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12.18;
52.08;
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TELEFAX: (703) 836-2021
INFORMATION FOR SED ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2095 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...us/KEY: CDS
; LOCATION: 156..2093
US-08-910-990-8
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Best Local Similarity
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;
;ENGTH: 2259
5185254-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
5185254-3
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1S-08-910-990-8/C

1S-08-910-910-8/C

1S-08-910-90-8/C

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                  OPERAITING SYSTEM: PC-DOS/NS-DOS
SOFTHARE: PC-DOS/NS-DOS
SOFTHARE: PC-DOS/NS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,230
FILING DATE: 16-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/110,736
FILING DATE: 23-MUG-1993
APPLICATION NUMBER: US 4-245950
FILING DATE: 24-MUG-1993
APPLICATION UNMBER: US 6-237118
FILING DATE: 06-MUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: CLANG-POSTE NUMBER: 36.113
REFERENCE/DOCKET NUMBER: 36.113
REFERENCE/COCKET NUMBER: 36.113
REFERENCE/COCKET NUMBER: 36.113
FILEDRONE: (703) 836-6620
INFORMATION PROBARATION:
TELECOMMUNICATION INFORMATION:
TELEPRONE: (703) 836-6620
INFORMATION PROBARES: 001560-215
TELEPRONE: APPLICATION PROBARTION:
TELEPRONE: 2095 BASE PALES
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: CDS
) LOCATION: 156..2093
US-08-405-230-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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67 CCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTT 126
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APPLICANT: LINNENBACH, ALBAN
TITLE OF INVENTION: GENE FAMILY OF TUMOR-ASSOCIATED ANTIGENS
NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/291,583
FILING DATE: 29-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29; DB 7; Length 2259; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 12.1%; Score 29; DB 3; Length 2095; Best Local Similarity 48.2%; Pred. No. 1.6; Matches 80; Conservative 0; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 AATTGCTTGAAAANTCTGCCTCCTCCTCCATCTCCCTTCAGGGACC 232
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Pactor of the lease #1.0, Version #1.25
SOFTWART APPLICATION DATA:
APPLICATION NUMBER: US/08/910,990
FILING DATE: 16-NAR-1995
APPLICATION NUMBER: US 08/405,230
FILING DATE: 16-NAR-1995
APPLICATION NUMBER: UP 4-245950
FILING DATE: 23-NGC-1993
APPLICATION NUMBER: UP 5-237118
APPLICATION NUMBER: UP 5-237118
APPLICATION NUMBER: UP 5-237118
APTORNEY AGENT INFORMATION:
NAME: CRADE-FOULY, Shalon E
RESISTAATION NUMBER: 36,113
REFERENCE/POCKER NUMBER: 36,113
REFERENCE/POCKER NUMBER: 001560-215
TELECHMUNICATION INFORMATION:
TELEPHONE: (703), 2000-200
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GENERAL INFORMATION:
APPLICANT: REGOAA, HISAO
APPLICANT: RECOAA, NAOHIKO
APPLICANT: TO, KAZUTOSHI
TITLE OF INVENTION: EXPRESSION VECTOR USING THE GENE
TITLE OF INVENTION: EXPRESSION REGULATING REGION OF THE ADP RIBOSYLATION
TITLE OF INVENTION: FACTOR
NUMBER OF SEQUENCES:
ADDRESSPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Patent No. 5935803

GENERAL INFORMATION:
APPLICANT: Dasquez, Nicki J.
APPLICANT: Ron, Dorit
APPLICANT: VOTONOVA, Anna F.
APPLICANT: Napolitano, Eugene W.
TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
TITLE OF INVENTION: USING COGNATE INTERACTION OF PRC-THETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 GCCACTATGGGGTCTGGGCTGCCCTTGTCCTCCTTGACCCTCCTTGG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 GCCAGCAGGCGCCTGGGCAGCCCTGGCCCCCTCTGGCCCATCTTCGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 STATE: VIRGINIA VIRGINIA STATE: VIRGINIA ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.5%; Score 27.6; DB 2; Length 3
Best Local Similarity 72.0%; Pred. No. 5.8;
Matches 36; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILIGO DATE: 07-APR-1995
CLASSIFICATION NUMBER: US/08/418,44A
FILING DATE: 07-APR-1995
APPLICATION NUMBER: US/08/418,44A
APPLICATION NUMBER: J80
PRIOR APPLICATION DATA:
APPLICATION NUMBER: J80
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: ODIOn, NO. 5773680mn F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2589-024-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICAT
     3932 GGCCTGGGCGCCTCGTTCTCCATCTAGGC 3903
                                                                                                                                                                                                                                                                US-08-418-444A-1/c
; Sequence 1, Application US/08418444A
; Patent No. 5773688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double
TOPOLOGY: 11near
MOLECULE TPE: DNA (genomic)
US-08-418-444A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-08-665-647-4
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     ö
                                                                                                                                                                                                                                                                                                  3992 CAGGGTCTCCGGTGTCGCCTTCATTCGAGGATGGCCCAGGGGGACCTGGGGGTCCAGGCG 3933
                                                                                                                                                                     Gaps
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0; Gaps
                                                                                                21 CTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCCTC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08494168
Patent No. 5731192
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhou, Jing
TITLE OF INVENTION: Collagen COL446: Gene, Protein and Method
TITLE OF INVENTION: of Detecting Collagen Deficiency
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5102;
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56.7%; Pred. No. 7.2;
tive 0; Mismatches 39; Indels
     60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIF: 20007-5109
ZIF: 20007-5109
COMPUTER READABLE FORM:
WEDIOW TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATURG SYSTEM: PC COMPATIBLE
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PULING DATE: 27-AUG-1993
ATTORNEY AGENT INFORMATION:
NAME: SARE, BENTARED D.
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION THORMATION:
TELECOMMUNICATION 1020572-5309
THERE AND THE AUGUST 
     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 CCCCTTGICCTCCTCTTGACCCTCCTTGGC 95
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.5%
Best Local Similarity 56.7%
Matches 51; Conservative
65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1240 aagga 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 AAGGA 145
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US-08-494-168-1/C
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; LOCATION:
US-08-494-168-1
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Matches
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US-08-485-449-1
Sequence 1, Application US/08485449
; Patent No. 5824789
GENERAL INFORMATION:
TILLE OF INVENTION: HEMATOPOLETIC GROWTH FACTORS, NUCLEOTIDE
TILLE OF INVENTION: THEREOF
TILLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ST
ADDRESSE: MORRISDN & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 TCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTGCAACTGAAGCTGAAGGAGT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   638 GGCCCGGCTACTCTGAGGGGACCGGCAGCTGCTGAAGCGCATGCTCATGCGGAAGCTGT 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 CITITCIGACAAATICCICCIAIGAGICCAGCIICCIGGAATIGCIIGAAAANICIGCCI 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           698 GTCAGCCACAGAATGCCACTACAGACTCCAGCCCGCCCGAGAGCATGGACGCTCTGCCT 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 ATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCTTGACCC 87
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                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTRARE: PREST TO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/08/665,647
FILINO BATE: 1B - JUN 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGHS, RATE H:
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22550-20025.25
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 892-0168
TELEFAX: (202) 892-1560
TELEFAX: (202) 892-1560
TELEFAX: 1294 Dass palis
TYPE: INCLEACE acid
TYPE: INCLEACE acid
TYPE: INCLEACE acid
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11near
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..1293
                                                                                                                                            COUNTRY: USA
ZIP: 20006-1888
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; LOCATION: 1..1
US-08-665-647-4
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COMPTER MARANAL PROPER LINE
COMPTER MARANAL PROPERTY PROPERTY
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120 ATGACTITGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGC 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD 1108 GTTCTTGAGACTCTTGATATTTCTGTCTTCTCCTTGTGTTTCTGAG 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thosessen, Hans Christian
APPLICANT: Thosessen, Hans Christian
APPLICANT: Thosessen, Michael
APPLICANT: Excerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 TICCIGGAATIGCTIGAAANICIGCCICCICCICCATCICCCTICAG 227
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: FEBTUARY 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: PAUL T. CLARK
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
2008-469-486-1
: Sequence 1, Application US/08469486
: Patent No. 5739281
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                     SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: NUCleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TBLYNOTOL
CLONE: 40194
US-08-878-989-9
           TELEFHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 225 Franklin STREET: 225 Franklin STREE: Boston STATE: Massachusetts COUNTRY: USA ZIP: 02110-2804 COMPUTER READABLE FORM:
                                                                                 TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 CCTCCATCCCAGGAGCGCAGTGGCCCACTATGGGGTCTGGGCTGCCCCTTGTCCTCTT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.4%; Score 27.2; DB 6; Length 3398;
49.3%; Pred. No. 8.2;
tive 0; Mismatches 73; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Golly, Neil C.
APPLICANT: Golly, Surya K.
APPLICANT: Goll, Surya K.
APPLICANT: Shah, Puryi
ITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CITY: Palo Alto
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 94304
COUPUTER READALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM DOS
SOFTWARE: FASTEM OF WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/878,989
FILING DATE:
CLASSIFICATION DATA:
APPLICATION UMBER:
FILING DATE:
FILING DATE:
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NAME: Billings, lucy J J
REGISIRATION NUMBER: 36,749
REFERENCE/COCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 GGAGTCTTTTCTGACAAATTCCTC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 GTACACCCCATTGTCTGTCTTC 394
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 496-824
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3398 DASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 49.39
Matches 71, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 121..2961
PCT-US95-08493-12
                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
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US-08-878-989-9/c
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Search completed: March 22, 2000, 01:22:29 Job time: 5633 sec

Run on:

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March 22, 2000, 04:46:59; Search time 802.03 seconds (without alignments) 1125.125 Million cell updates/sec
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239
1 GGCCACCGGGACTTCAGTGT......CCCTTCAGGGACCAGCGTCA 239
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                4538634 seqs, 1887831982 residues
                                                                            OM nucleic - nucleic search, using sw model
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1: em_est1:*
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9b est131:* em_est23:*	9 9 9 9
	25,35
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AI857998 w169b01.x	AQ718761 HS 5511 B	AI136523 UI-R-C2p-	AQ838514 HS_5011 A	F06958 HSC10C101 n	AA376266 EST88915	AA769782 ah71b05.s
а	AI857998	AQ718761	AI136523	AQ838514	F06958	AA376266	AA769782
8	61	83	42	88	7	32	38
% Query Match Length DB ID	404	552	328	509	348	238	412
Query Match	49.4	31.1	56.6	14.9	14.6	14.4	14.4
Score	118	74.4	63.6	35.6	35	34.4	34.4
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1...404
//Organism=Homo sapiens"
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//Olone="INAGE:2408041"
//Clone="INAGE:2408041"
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//Clone="INAGE:2408041"
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//Clone="INAGE:2408041"
//Clone="INAGE:2408041"
//Ab_host="Squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
metastatio,"
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//
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability. please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ718761 552 bp DNA GSS 13-JUL-1999 HS-551_B2_F09_T7A RCIT-11 Human Male BAC Library Homo sapiens qenomic clone Plate-1087 Col-18 Row-L, genomic survey sequence AQ718761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 CAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCT 168
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
High Throughput Sequencing Center
1010 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Exa: (206) 616-3887
Exa: (206) 616-3887
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Best Local Similarity 97.7%; Pred. No. 7.3e-25;
Matches 129; Conservative 0; Mismatches 2;
      Seg primer: -40UP from Glbco
High quality sequence stop: 395.
Location/Qualifiers
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Mammalia; Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Mammalia; Eukaryota: Primates; Catarrhini; Mominidae; Homo.

I (bases I to 404)

I (bases I to 404)

S. NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Tatitute, Cancer Genome Anatomy Project (CGAP),
Tunor Gene Index

U Opublished (1997)

On Jun 5, 1998 this sequence version replaced gi:3189004.

Contact: Robert Strausberge, Ph.D.
Tel: (301) 496-1550

Emmal: Robert Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. and Solars, Ph.D.
CONA Library Preparation: M. Bento Soars, Ph.D.
CONA Library Arrayed by: Greg Lennon, Ph.D.
CONA Library Arrayed by: Greg Lennon (Stribution information can befound through the I.M.A.G. E. Consortium/Link at:
www-blo.linl.gov/bbrp/image/image/image.html
A1632159 ts85e12.x
A1607352 tc42hll.x
AN009894 ws88h09.x
AN078074 fe24b05.y
AN78074 fe16b05.y
F08745 HSC1DB011.x
AN18453 fe16b05.y
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AA555402 CITRI-E1-AA50491 habxb0037C
AA555402 CITRI-E1-AA50491 habxb0037C
AA55402 CITRI-E1-AA50494 Habxb0037C
AA55404 Habxb0037C
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AA55414 tf76d10.x
AA55414 tf76d10.x
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AA55414 tf26d10.x
AA554140 sm58e05.s
AA55414 tf26d10.x
AA55416 tf26d10.x
AA56416 tf26d10.x
AA55416 tf26d10.x

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W169bOl.xl NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408041 3',
mRNA sequence.
AI857998.1 GI:5511614
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CNS00DED
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A1810515
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RESULT 1 A1857998/C LOCUS DEFINITION

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REFERENCE AUTHORS TITLE

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The sequence tag present in the cDNA between the NotI site and the Oligo-dr track served to identify it as a clone from the normalized adult Lung library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
blate: 1087 row: L column: 18
Seq primer: T7
Class: BAC ends
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Rattus norvegicus
Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Mammalla;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Murinae;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases I to 328)
Bonaldo, M.F., Lenon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
153 c 124 g 117 t 17 others
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UI-R-C2p-nq-e-02-0-UI.sl UI-R-C2p Rattus norvegicus cDNA clone
UI-R-C2p-nq-e-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 AACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTC 166
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Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 552;
                                                                                                                                                                                                           High quality sequence stop: 552.
Location/Qualifiers
1. 552.
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=1087 Col=18 Row=L"
/clone=lib="RRCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
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/lab_host="DH10B (Life Technologies)"
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87.1%; Pred. No. 6.3e-12;
tive 0; Mismatches 12;

    .328
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    /db_xref="taxon:10116"

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/note="vector: pT73D-Pac (Pharmacia) with a modified polyliker; Site_1: Bco Ri; The UI-C2p plubrary is a subtracted library derived from the UI-C2p library, which is a subtracted library derived from the UI-R-C1 library, which is a subtracted library of size in UI-R-C0 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C2p) was constructed as follows: PCR amplified cDNA inserts from UI-R-C1 clones from which 3' ESTS had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles. The remaining single-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UI-R-C2P library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 77 c 98 g 91 t
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia;
Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 509)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 GCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 TGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAA-NTCTGCCTCCTCC 212
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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Pred. No. 7.9e-09;
0; Mismatches 45; Indels 1
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High Throughput Sequencing Center
University of Washington
410 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 TCCACCTCTCACGGGGACCAATGTCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 TCCAICTCCCTTCAGGGACCAGCGTCA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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A0838514.1 GI:5808388
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Best Local Similarity
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Other ESTS: THC191210
Contact: Kerlavage, AR
Bioinformatics
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ORIGIN
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AUTHORS
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COMMENT
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KEYWORDS
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                                                          FEATURES
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(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plater: 587 row: G column: 20
Seg primer: Sp6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryofa, Metszoa; Chordats; Craniata, Vertebrata; Mammslia; Butheria; Primstes; Catarrhini; Hominidae; Homo.

[ (bass 1 to 348.)

Auffrsy,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprst,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
LOTENCO,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebsstiani-Ksbaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 127 c 106 g 153 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F06958 348 bp mRNA EST 20-FEB-1995 SESCIOL101 normslized infant brain cDNA Homo sapiens cDNA clone c-1qc10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 GIGACCICINITICICCICACCCCAIGGICTCICAGGAGGAGGAGCAGGIGGCITITCIIIC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 CCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-lqcl0
Insert Length: 639 5td Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Sep 21, 1992 this sequence version replaced g1:278976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genethon Centre de recherche sur le Genome Humain
1.rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 14.9%; Score 35.6; DB 88; Length 509; Best Local Similarity 47.3%; Pred. No. 1.8; Matches 104; Conservative 0; Mismatches 116; Indels 0
                                                                                                                                                            High quality sequence stop: 509.
Location/Qualifiers
1 .509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 ATTCCTTGAAANTCTGCCTCCTCCTCCATCTCCCTTCAG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 Arccraccracacracaccaccaccrcracac 299
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Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Genethon
Genexpress-Genethon
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KEYWORDS
SOURCE
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MEDLINE
COMMENT
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/star_repe="total brain"
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/dev.stage="3 months old"
/dev.stage="3 months old"
/dev.stage="3 months old;
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/dep.stage=1 months old;
/dep.stage=2 months old;
/dev.stage=3 mo
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Eutheria: Primates; Catarrhini; Hominidae; Homo.

I (basea; 1 to 238)

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocsyne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.D., Fuldher, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Relley, J.C., Liu, L.I., Marmeros, S.M., Meristok, J.M., Relley, J.M., Relley, J.M., Robonald, L.A., Nguyen, D.T., Pelligino, S.M., Phillips, C.A., Ryder, S.E., Otterback, T.R., Weidman, J.F., Lil, Y., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Lil, Y., Brings, T.D., Feng, D.F., Ferrison, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Peng, D.F., Ferrison, M.A., Coleman, T.A., Collins, E.J., Kozak, D.L., Kunsch, C., Hugjun, J., Li, H., Weissner, P.S., Olsen, H., Fisser, C., and Charle, J.M., Racelline, W.A., Fields, C., Fisser, C., M., and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA376266 238 bp mRNA EST 21-APR-1997
21-APR-1997 L Cells II Homo sapiens CDNA 5' end, mRNA sequence.
AA376266.1 GI:2028809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 2.3;
0; Mismatches 31; Indels
                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone=lib="normalized infant brain cDNA"
/sex="Female"
Seq primer: (-21)M13_universs1
High quslity sequence stop: 150.
Location/Qusliflers
1. .348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 63.1
Matches 53; Conservative
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/note-"Vector: pt773D-Pac (Pharmacia) with a modified Polylinker, Site_1: Not I, Site_2: Eco RI: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINI at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIG32159 458 bp mRNA EST 26-APR-1999
t4885el2.xl NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:2238094 3',
AIG32159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Bubharla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 458)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 TGTTGCCTCCCTCCCAGGATCCCTTTGGTGATATGGTGTTCAGGATGCACCACCACCACCAC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 TGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCCTTGTCCTC 77
                                                                                                                                                                                                                                                                                                                                                                                                                         14.4%; Score 34.4; DB 38; Length 412; llarity 63.1%; Pred. No. 3.7; Conservative 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:2238094"
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                                            /clone_lib="Soares_testis_NHT"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40UP from Gibco
High quality sequence stop: 439.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 CTCTAGATACCTTCAGGCAACACA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 CTCTTGACCCTCCTTGGCAGCTCA 101
                       /clone="1321041"
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                                                                                                                                                                                             primer [5
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Best Local Similarity
Matches 53; Conserv
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A1632159/c
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
www-bio.llnl.gov/bbrp/image/image.html
The Institute for Genomic Research
912 Medical Center Drive, Rockville, ND 20850 USA
71: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
Enail: arkerlav@tigr.org
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primar: Mi3 Revorse.
Location/Qualifiers
1...238
                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="ATCC (inhost):180944"
/db_xref="ATCC (inhost):180944"
/db_xref="taxon:9606"
/clome_lib="HSC172 cells II"
/cell_type="fibroblast"
/cell_type="fibroblast"
/dev_stage="fetal"
/note="Organ: lung; Vector: pBluescript SK-; Site_1:
BCORI; Site_2: XhOI*
8 a 70 c 50 g 66 t 4 others
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1 (bases 1 to 41)

NCI-GAP http://www.ncbl.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA769782 412 bp mRNA EST 29-DEC-1998
ah71b05.sl Soares_testis_NHT Homo sapiens cDNA clone 1321041 3',
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Tunor Gene Index
Unpublished (1997)
On Jan 9, 1999 this sequence version replaced gi:936203.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Enail: Robert_Strausbergenih.gov
CONA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 238;
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14.4%; Score 34.4; DB 32; Length
Best Local Similarity 63.1%; Pred. NO. 3;
Matches 53; Conservative 0; Mismatches 31; Indels
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 402.
Location/Qualifiers
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/db_xref=?taxon:9606"
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a modified polylinker; Site] Not I: Site_2: Eco R:
gral amounts of plasmid DNA from three normalized
Libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified CDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E clones 297480-302087, 682632-687239,
S75408-728711, and 729096-31399. Subtraction by Bento
Scares and M. Fatina Bonaldo.
                                                                                                                                                                                                                                                                                                                                            AI807980 513 bp mRNA EST 07-JUL-1999 wf44cl1.xl Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358452 3' similar to SW:C212_HUMAN 043822 28.3 KD PROTEIN C210KF2; contains MER22.bl MER22 repetitive element ;, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 513)
Mri-GAP http://www.ncbi.nlm.nih.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -400P from Gibco. High quality sequence stop: 325. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CCACCGGGACTICAGIGICICCICCATCCCAGGAGGGCGCAGIGGCCACIAIGGGGTCIGGG 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ompublished (1997)
On Jun 5, 1998 this sequence version replaced g1:3188813.
Contact: Robert Strausberg, Ph.D.
Email: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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     Length 470;
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55.2%; Pred. No. 12;
tive 0; Mismatches 52; Indels
Ouery Match
Best Local Similarity 63.1%; Pred. No. 3.9;
Matches 53; Conservative 0; Mismatches 31; Indels
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156 c 144 g 109 t
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                         78 CTCTTGACCCTCCTTGGCAGCTCA 101
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AI807980.1 GI:5394637
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Best Local Similarity 55.28
Matches 64; Conservative
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A1807980/c
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Bukaryota Metazoa, Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhin; Hominidae; Homo.
I (bases 1 to 470)
NCI-GGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NRI-GGAP institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tunor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:ll34312.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 46-L1550
Email: Robert_Strausberg@ih.gov
This clone is available royalty free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI803529 470 bp mRNA EST 06-JUL-1999 tc42hil.xl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2067333 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                              Score 34.4; DB 49; Length 458;
Pred. No. 3.8;
0; Mismatches 31; Indels 0;
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^Organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="inhaGE:2067333"

/clone="inhaGE:2067333"

/clone="inhaGe:2067333"

/clone="inhaGe:2067333"

/dev_stage="8-9 weeks"

/lab_host="BH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 CTCTAGATACCTTCAGGCAACACA 233
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AI803529.1 GI:5368989
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Best Local Similarity 63.1%;
Matches 53; Conservative (
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/db_xref="taxon:9606"
/dlone="InhGE:250809"
/dlone="InhGE:250809"
/dlone="Liph="NatZ_250809"
/dlose="Liph="Arganization"
/dlose="Yector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco Ri; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - ollgo(dT) primer. Double-stranded cDNA
was prepared to Eco RI adaptors (Pharmacia), digasted with Not
I and cloned into the Not I and Eco RI sites of the
modified pT713 vector. Library went through one round of
notice of RI sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arraying: Gerg Lennon, Ph.D.

DNA Sequencing by: Mashington University Genome Sequencing Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

WWW-blo.llnl.gov/bbrp/image/image.html
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1 (bases 1 to 360; NCT-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.

NCT-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                  Tunor Gene Index
Unpublished (1997)
On Mar ID, 1998 this sequence version replaced gi:2948428.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
                                                                                                      AW009894 360 bp mRNA EST 10-SEP-1999
WERBAD9.x1 NCI_CGAP_CG3 HOMO Sapiens CDNA clone IMAGE:2505089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 ATACAAGAGITGAGGIGTCCAAGCTITAGCITAAGCIGTATCIGITATTAGGATIGAAIC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 TCCTIGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAGGAGT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 CITITCIGACAAAITCCICCIAIGAGICCAGCITCCIGGAAIIGCITGAAAANTCIGCCI 207
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226 CAGCCCCGGCCCCACACACGCCCTCCCGGCTTTCCCAAATCGTTCCAGGACAGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 63; Length 360;
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Pred. No. 12;
0; Mismatches 100;
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Location/Qualifiers
                                                                                                                                                                                  AW009894.1 GI:5858672
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1 Similarity 47.9%;
92; Conservative
                                                                                                                                            mRNA sequence.
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                                                                                                                                                                                                                                                Homo sapiens
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil; Neopterygil; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 537)

1 (Cases 1 to 537)

1 (Cark, M., Obnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba; H., Marlin, J., Boekch, T., Waller, T., Underwood, K., Steptoe, M., Thaising, B., Allen, M., Bowers, Y., Rerson, R., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Wilson, M., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Wilson, T., Jackson, Y., Cardenas, M., McCann, R., Washi Lebrafish Est Project 1998

Unpublished (1998)

On May 18, 1998 this sequence version replaced gl:3136840.

Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Tex: 314 286 1810
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/lab_host="Xil-blue MRF"
//tote="Vector: pSPORT; Site_l: NotI; Site_2: Sall: 1st
strand cDNA was prinned with a Not I - oligo(dT)15 primer
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and Cloned into the Not I and Sal I
sites of the pSPORT! vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab: ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Bellin). CDNAs for EST
analysis were selected following oligonucleotide
bybridization fingerprinting of arrayed clones from
cenbryonic shield stage (5.6 h) libraries. Fingerprint
single cDNA from each cluster was chosen for sequencing
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark DNA Sequencing by: washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.respen.com) (email contact: Info@respen.com) and
RessourcectEentrumPrimarDatenbank, Berlin, Germany (web address:
AW078074 537 bp mRNA EST 14-OCT-1999
fe24b05.y1 zebrafish WashU MPIMG EST Danio rerio cDNA 5', mRNA
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Seq primer: T3 ET from Amersham
High quality sequence stop: 498.
Location/Qualifiers
1. 537
/organism="Danio rerio"
/db_xref="texon:7955"
/clone_lib="Zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
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Seg primer: (-21)Mi3_universal
High quality sequence stop: 277.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                        13.6%;
56.6%;
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                                                                                                                                                                                               133 c
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Best Local Similarity 56.6'
Matches 60; Conservative
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Budrayota: Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Budrayota: Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Budrayota: Metazoa; Eleostai; Buteleoatei; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.

C 1 (basea; Lo 523)

C 2 1 (basea; Lo 523)

Eleosta, Julilear, L., Kucaba, T., Martin, J., Back, C., Wylke, T., Ederwood, K., Steptoe, M.; Mathain, B., Allon, M.; Bowers, T., Underwood, K., Steptoe, M.; Theising, B., Allon, M.; Bowers, T., Ritter, E., Rohn, S., Shin, T., Jackson, Y., Cardenas, M.; McCann, R., Washu Zebrafish Est Project 1998

Unpublished (1998)

On Dec 20, 1995 this sequence version replaced gi:ll34195.

Other_ESTS: felbobs.xl

Contact: Stephen L. Johnson
Washington University School of Medicine
Small: Stafish@wataon.wustl.edu
Contact: Stephen L. Johnson
Mathaw Clark DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louia,
Massouri (web address: www.resgen.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Ressourcembank, Berlin, Germany (web address:
Rescourcembank, Berlin, Germany (web. address:
Rescourcembank, Berlin, G
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AW128453 523 bp mRNA EST 25-OCT-1999
fel6b05.yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5', mRNA
                                                                                                                                                                  456 AGAGIGGAAGICATIAAGGAGGCIGAGCAGACCTITICCATCICCIGAACATCAGAGAC 397
                                                         Gaps
                                                                                                            36 AGCGCAGTGGCCACTATGGGGTCTGGGCTGCCCTTGTCCTCCTTGACCCTCCTTGGC 95
                                                      ö
DB 64; Length 537;
                                                         Indels
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/organism="Danio rerio"
/db.xref="taxon:7955"
/clone_llb="zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                                                                                                                                                                                                                     396 ATCTGTGAGAAACGAGTGCTGGATGTGGCTTGACTGTTACTCTTA 351
                                                         46;
Score 32.4; DB;
Pred. No. 16;
0; Mismatches
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Location/Qualifiers
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AW128453.1 GI:6116357
      13.6%;
56.6%;
                                   Local Similarity 56.6
les 60; Conservative
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Danio rerio
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AW128453/c
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/tissue type="total brain"
/tissue type="total brain"
/dos="organ: Jamonths old"
/force="organ: brain; Vectors is a family sold;
Site_2: Not1: Sex=Female; dev_stage=3 months old;
Site_2: Not1: Sex=Female; dev_stage=3 months old;
Isolate=muscular atrophy patient; tissue_type=total
brain; total mRNN was oligo-(dn) primed and directionally
cloned 5' -> 3' into the Hindili -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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INAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rus745 339 bp mRNA EST 20-FEB-1995
HSC1DB011 normalized infant brain cDNA Homo sapiens cDNA clone
c-1dbb1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 AGAGTGGAAGTCATTAAGGAGGTGAGCAGACCCTTTTCCATCTCCTGAACATCAGAGAC 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; primates; Catarrhini; Hominidae; Homo.
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Genethon Centre de recherche aur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Sep 21, 1992 this aequence version replaced gl:279421
Contact: Genethon
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 69; Length 523;
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/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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; Pred. No. 16;
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/db_xref="taxon:9606"
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 742)

S Nori(C., Albanese, V., Lebre, A.S., Holbert, S., Saada, C., Gudjueleret, L., Masart, C., Gudjilou, S., Gervy, P., Poulier, P., Maissant, C., Gudjilou, S., Gervy, P., Poulier, E., Rigault, P., Meissenbach, J., Lennon, G., Chumakov, I., Dausset, J., Lehrach, H., Cohen, D. and Cann, H.M.

Survey of CAG/CTG repeats in human cDNAs representing new genes: candidates for inherited neurological disorders

L Hum. Mol. Genet. 5 (7), 1001-1009 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                  278408 742 bp mRNA EST 28-JUL-1999
HSZ78408 Human fetal brain S. Meier-Ewert Homo sapiens CDNA clone
3.99 (CEPH), mRNA sequence.
278408
Normalization_method:
                                                                                                                                                                                                                        61 CCACTGCGCTGGTGTCTCCTGCCCCTCGGAAGCTTGGATGCCCCTNCACACCCTCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 GGCTACTCCTAGGGATAAGCCCCCGGTCCCTCATCCCTGGTCAGTGTCCCTGACCCCCA 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Journal 14, 1993 this sequence version replaced gi:837709. Contact: Neri C.
Fondation Jean Dausset - CEPH
27 Rue Juliette Dodu, 75010 Paris, France
ICRF clone ID ICREPSOTU04199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                 Query Match 13.5%; Score 32.2; DB 21; Length 339; Best Local Similarity 58.5%; Pred. No. 15; Matches 55; Conservative 0; Mismatches 39; Indels 0
                                       2 others
Dept. Columbia University, USA.
Bento Soares, P.N.A.S in press*
116 c 100 g 64 t
                                                                                                                                                                                                                                                                                 83 GACCCTCCTTGGCAGCTCACATGGAACAGGGCCG 116
                                                                                                                                                                                                                                                                                                    Z78408.1 GI:1495181
                                       57 a
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COMMENT
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KEYWORDS
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Search completed: March 22, 2000, 05:09:43 Job time: 1364 sec

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Mon Mar 20 12:32:52 2000; MasPar time 5.78 Seconds 319.798 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-092-296-15 (1-78) from USO9092296.pep 558 1 MGSCLPLVLLLTLGSSHGT.....SGTSVTLHHARSQHHVVCNT 78 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35 1:geneseqp

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 27.552; Variance 131.690; scale 0.209

SUMMARIES

1		ъ						
No.	Score	Query	Length	DB	£ £	Description	Pred. No.	
1	558	100.0	78	-	W88498	Human stomach carcinom	3.436-38	
~	98	15.4	46	Н	W7 03 27	Secreted protein FB78	4.56e+01	
m	86	15.4	47	н	W73408	Human secreted protein	4.56e+01	
4	82	15.2	325	Н	R48730	G-protein coupled bovi	5.33e+01	
Ŋ	82	15.2	325	Н	W02702	G-protein coupled bovi	5.33e+01	
Q	84	15.1	154	Н	W98259	H. pylori GHPO 895 pro	6.24e+01	
7	84	15.1	795	Н	W97842	Human P2Y11 receptor.	6.24e+01	
ω	83	14.9	194	Н	R47338	Peptide fragment of te	7.29e+01	
σ	83	14.9	411	Н	W57046	Mouse apoptosis induci	7.29e+01	
10	85	14.7	110	Н	R26954	Human I lymphocyte rec	8.52e+01	
11	82	14.7	169	Н	W21674	Human mitochondrial el	8.52e+01	
12	81	14.5	401	Н	W59924	Human 7-transmembrane	9.94e+01	
13	81	14.5	1253	Н	W10038	Mad binding protein, m	9.94e+01	
14	81	14.5	1261	Н	W10040	Mad binding protein, m	9.94e+01	
15	80	14.3	398	Н	R15138	Human serotonin 1D rec	1.16e+02	
16	80	14.3	713	Н	R10052	Cyclomaltodextrin gluc	1.16e+02	
17	80	14.3	713	Н	R06110	Sequence of cyclomalto	1.16e+02	
18	80	14.3	945	Н	R66060	Human NMDAR2 receptor	1.16e+02	
19	80	14.3	1214	Н	R66065	Human NMDAR2 receptor	1.16e+02	
50	80	14.3	1214	Н	W87509	Human N-methyl-D-aspar	1.16e+02	
21	80	14.3	1219	Н	W87507	Human N-methyl-D-aspar	1.16e+02	
22	80	14.3	1219	Н	R66063	Human NMDAR2 receptor	1.16e+02	
23	80	14.3	1231	Н	R66062	Human NMDAR2 receptor	1.16e + 02	

24 80 14.3 1231 1 W87506 Human N-mer 25 80 14.3 1236 1 R66637 Human N-mer 27 80 14.3 1239 1 R66034 Human N-mer 27 80 14.3 1239 1 R66034 Human N-mer 28 80 14.3 1239 1 R6604 Human N-mer 28 80 14.3 1239 1 R6604 Human N-mer 29 80 14.3 1244 1 W87505 Human N-mer 29 80 14.3 1244 1 W87505 Human N-mer 20 80 14.3 1244 1 W87505 Human N-mer 20 31 79 14.2 1244 1 W87505 Human N-mer 20 32 79 14.2 969 1 W49879 Human n-crowday 14.2 969 1 W49879 Human n-crowday 14.2 969 1 W25170 Human insurance 23 77 9 14.2 1015 1 W18032 The Profit of 14.2 1015 1 W18032 Human secretary 14.0 120 1 R9783 Human protts 39 78 14.0 120 1 R9783 Human secretary 14.0 120 1 R9783 Human secretary 14.0 120 1 R9783 Human secretary 15.0 Human; stomach carcinoma HP10406-encoded transmembrane protein; HP10408; human; stomach carcinoma HP10408; human; stomach carcinomy FR No-DEC-1998 (SAGAM CHRH RES CENTRE) RW M88498 Standard; Protein; HP10408; human; stomach carcinomy FR No-DEC-1998 (SAGAM CHRH RES CENTRE) RW M88498 Standard; Protein production; gene diagnosis, and proteins containing transmembrane domain for carcinomy of proteins encoded protein production of a novel transmembrane domain stomach carcinomy of proteins encoded protein production of proteins encoded by vectors containing stomach carcinomy encoded by human stomach carcinomy HP No-HP HP N-HP N-HP N-HP N-HP N-HP N-HP N-H	Human N-methyl-D-aspar 1.16e+02 Human N-methyl-D-aspar 1.16e+02 Human N-methyl-D-aspar 1.16e+02 Human NmChALZ receptor 1.16e+02 Human NmChALZ receptor 1.16e+02 Human NmChALZ receptor 1.16e+02 Human NmChALZ receptor 1.16e+02 Human NmChALJ-D-aspar 1.16e+02 Human cros induced gr 1.35e+02 Human insulinoma-assoc 1.35e+02 Human insulinoma-assoc 1.35e+02 Human protein tyrosine 1.35e+02 Human protein tyrosine 1.35e+02 Human secreted protein 1.58e+02 Kaposi's sarcoma assoc 1.58e+02 C-Delta-1 polypeptide 1.58e+02 Claitamydia pneumoniae s 1.58e+02 Clutamydia pneumoniae s 1.58e+02 Human screted protein 1.58e+02 C-Delta-1 polypeptide 1.58e+02	GOMENTS GOMENTS GOMENTS Re-encoded transmembrane protein. Human; stomach cancer. Transmembrane domains and their transmembrane domains and their the preparation of antibodies and ish. To an ovel transmembrane protein to a novel transmembrane protein to a novel transmembrane protein trons alone and a putative The invention provides nucleotide The invention provides nucleotide The invention provides nucleotide and for all transmembrane proteins aning for 18 transmembrane proteins aning such polynucleotides, and tevetors. The polynucleotides can be used and as gene sources for gene therapy proteins encoded by the oDNA. The tection of liquads corresponding to te screening of low mol.wt. medicines.
44444444444444444444444444444444444444	W87506 R66037 W87508 R66061 R66061 R66061 W14993 W21171 W21711 W21171 W2171 W2171 W2171 W2171 W2171 W2171 W2171 W2171 W2171 W2171 W2171 W2171 W2171 W2171 W2171 W21	AA. AA. (108 - encc (108 - e
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Score 558; DB 1; Length 78; Pred. No. 3.43e-38; 0; Mismatches 0; Indels 0; Gaps Query Match 100.0%; Best Local Similarity 100.0%; Matches 78; Conservative

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Human secreted protein encoded by Gene No. 12.

Secreted protein, human; protein therapy; gene therapy; blood disorder; pathological condition; diagnosia; cancer; neurological disorder; developmental abnormality; foetal deficiency; leukaemia; hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schizophrenia; prostate disease; autoimmune disorder; AlDS.
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/note= "predicted leader/signal sequence, or transmembrane domain"
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                                                                                                                                                                                                                                 25-FEB-1998; U03697.
24-FEB-1998; US-028724.
26-FEB-1997; US-805819.
(GENY ) GENETICS INST INC.
Radio LM, Spaulding V, Treacy M; WPI; 98-481139/41.
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                                                                                                                                 Location/Qualifiers
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                                                            21-DEC-1998 (first entry)
Secreted protein FB78_1.
Secreted protein; DU123_1; human.
Homo sapiens.
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W73408 standard; Protein; 47 AA.
              .r 2
W70327 standard; Protein; 46 AA.
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28-MAY-1998. U10868.
29-AUG-1997. US-056296.
30-MAY-1997; US-044039.
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                                                                                                                                                 Peptide
              RESULT
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New isolated human genes - useful for diagnosis and treatment of, e.g. cancers, neurological disorders, immune diseases, developmental production disorders or blood disorders.

Fig. cancers or blood disorders immune diseases, developmental production disorders or blood disorders in man secretal protein, and is cancers or large sequence represents a human secretad protein, and is expressed in activated neutorphils, endothelial cells, T-cells and concerns are expressed in activated neutorphils, endothelial cells, T-cells and concerns of the invention and their corresponding accreted protein or an esser extent in brain and liver.

The DNA sequences of the invention and their corresponding accreted protein or gene therapy. Also pathological conditions or grample or grample or greening the mount of the new polypeptides in a cambe diagnosed by determining the amount of the new polypeptides in a cambe of adamosed by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded conclude developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal caficienties, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic diseases, autoimmune conjuscing partners.

Sequence 47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARAPEL 1993; U08528.

PR 10-SEP-1993; U08528.

PR 10-SEP-1992; U08528.

PR 10-SEP-1993; U08528.

PR 10-SEP-1993; U08528.

PR 10-SEP-1993; U08528.

PR 10-SEP-1993; U08528.

PR 10-SEP-1992; U08528.

PR 10-SEP-1993; U08528.
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                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                      HUMAN GENOME SCI INC.
CC, Dillon PJ, Endress GA, Feng P, Ni, Ruben SM, Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R48730 standard; Protein; 325 AA. R48730;
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30-MAY-1997; US-048101.
30-MAY-1997; US-048190.
30-MAY-1997; US-050935.
29-MG-1997; US-056250.
29-AUG-1997; US-056250.
(HUMA-) HUMAN GENOME SCI
Carter KC, Dillon PJ, Enc
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Ruben SM
WPI; 99-070209/06.
N-PSDB; V08822.
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WO9405695-Al.
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Matches
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New dopamine receptor peptide - useful as antipsychotic agent, e.g.

New dopamine receptor peptide - useful as antipsychotic agent, e.g.

PT for treating schizophrenia

Disclosure; column 129-132; 184pp; English.

Proteins W02657-W02730 represent a range of G-protein coupled receptor

CGFN proteins sclienced from CAMP, adenosine, muscarinic acetylcholine,

adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopain, opsin,

codorant, cytomegaloviral and other GPR proteins. The receptor proteins

codorants, for use in G-protein coupled receptor ligand binding assays.

The polypeptide fragments retain biological activity such as binding assays.

CFN ligand or modulating GPR ligand binding to a GPR (see W02747-W02999)

CFN cramples of polypeptide fragments). The polypeptide fragments can

crample to a GPR abnormality e.g. a psychotic disorder such as
Polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mystally (first entry)
H. pylori GHPO 895 protein.
GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
GHPO protein; Helicobacter disease.
Helicobacter pylori.
Mysgala18-A.
MOG-OCT-1998; U06371.
29-JUL-1997; US-902515.
24-JUL-1997; US-881227.
24-JUN-1997; US-881227.
                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                  13-NOV-1996 (first entry)

Deprotein coupled bovine adrenal angiotensin II type-1 receptor.

G-protein coupled receptor; ligand blinding assay; transmembrane domain; schizophrenia; dopamine; cAMF; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin; odorant; cytomegalovirus; serotomergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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                                                                                            Score 85; DB 1; Length 325;
Pred. No. 5.33e+01;
5; Mismatches 8; Indels
                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 85; DB 1; Length 325;
Pred. No. 5.33e+01;
5; Mismatches 8; Indels
                                                                                                                                                                  23
                                                                                                                                                                                      34 FLINSSYESSFL-EL-LEKICLILHIP 58
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                                                                                                                                                          27 YMKLKTYASVFLLNLALADLCFLLTLP
                                                                                                                                                                                                                                                  .r 5
W02702 standard; peptide; 325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 YMKLKTYASVFLLNLALADLCFLLTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W98259 standard; Protein; 154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1996.
10-SEP-1992; 943236.
10-SEP-1992; US-943236.
09-SEP-1993; US-118270.
(UINY ) UNIV NEW YORK STATE.
                                                                                           Match 15.2%;
Local Similarity 44.4%;
Les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 15.2%;
Best Local Similarity 44.4%;
Matches 12; Conservative
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                                                        325 AA;
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New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases (Claim 8; Page 250-251; 2054pp; English.

This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroindomal diseases associated with these infections, including acute, chronic, and atrophic gastriis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                             Human P2III receptor.
P2III; G protein coupled receptor; human; infection; neutropaenia; agranulocytosis; cancer; leukaemia; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                               /note= "putative protein kinase C phosphorylation site"
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "calmodulin-dependent protein kinase phosphorylation site"
                                                                                                                                                                                      Score 84; DB 1; Length 154;
Pred. No. 6.24e+01;
5; Mismatches 12; Indels
                                                                                                                                                                                                              12; Indels
(INWR ) MERIEDY ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawl A, Kleanthous H, Miller C, Comen RP, Tomb J;
WPI; 98-54229746.
N-PSDB; X13978.
                                                                                                                                                                                                                             74 LGFGFGLGLGLGFVTSFLGSSFFGSSFL 105
                                                                                                                                                                                                                                            14 LGSSHGTGPGMTLQLKLKESFLTNSSYESSFL 45
                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-glycosylation"
794
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualiflers
                                                                                                                                                                                                                                                                                  RESULT 7
ID W97842 standard; Protein; 795 AA.
                                                                                                                                                                                     Query Match
Best Local Similarity 46.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                        W97842;
07-JUN-1999 (first entry)
                                                                                                                                                       detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boeynaems J, Commun1 D; WPI; 99-120876/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP-870101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-1997; EP-870101
(EURO-) EUROSCREEN SA.
                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-1999.
09-JUL-1998; BE0108
                                                                                                                                                                                                                                                                                                                                                                                 Modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                  Mod1fied_site
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified_site
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Gaps

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Sequence Query Match

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Matches

셤 ô RESULT

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transmembrane protein, useful for regulating cell death

Claim 16; Page 33-35; 45pp; Engilsh.

This sequence is the mouse apoptosis inducing receptor (AIR) of the
Invention. AIR is a Type I transmembrane protein, soluble forms of which
anneation. AIR is a Type I transmembrane protein, soluble forms of which
can be used to regulate cell death in a therapeutic setting. Soluble AIR
can also be used in vitro to block apoptosis or AIR-expressing cells, or
to screen agonists or antagonists of AIR activity. The cytoplasmic domain
of AIR can be used to develop assays for inhibitors of AIR-induced cell
death, which is useful to regulate cell death in a therapeutic setting as
well as in vitro. Agonists of AIR activity can be used to Aill tumour
cells that express AIR, or T cells expressing AIR in autoimmune diseases.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 35; 65pp; French.

Craimers, then amplified by anchored PCR using C-alpha specific primers, then amplified again using a different C-alpha specific primer. The amplified product was Sacir-restricted, inserted into Bluescript SK+ vector and used to transform E.coli XL7-blue.

Transformants were screened with a C-alpha specific probe and DNA from positive clones was sequenced in the C-slpha region. The sequence designated "IGR a 12" comprises the complete coding region of a gene of the subfamily V shpha 22; this subfamily was previously identified by the partial sequence (113pp) AC9 (Klein, M. H., Chen, N. H., Proc. Natl. Asad. Sci. USA 84:6884, 1987). The peptide encoded to the control of the subfamily value of the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequences and their monoclonal antibodies and oligo:nucleotide primers - encode variable alpha-chain regions of human T-lymphocyte receptors, for studying immune responses and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNYSPGLVSLILLLGRIRGDSVTQMEGPVTLSEEAFLTINCTYTATGYPSLF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Heighty-electricsshorg-pomilolkike-sfle-nssy-essfleel 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W21674 standard; Protein; 169 AA.
W21674;
29-5EP-1997 (first entry)
Humsn mitochondrial electron transport chain subunit CII-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 82; DB 1; Length 110;
Pred. No. 8.52e+01;
12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human T lymphocyte receptor V-alpha22 segment.
TCR; IGR a 12; variable region; immune system modulation;
T cell subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 83; DB 1; Length 411;
Pred. No. 7.29e+01;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ROUS ) ROUSSEL-CCLAF.

Perradini L, Hercend T, Roman-roman S, Triebel F;
WPI, 92-300035/36.

WFSDB, Q28129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R26954 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 LPLILLLLLGGQGGG-GMS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
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Local Similarity 34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                              h 14.9%;
Similarity 57.1%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LPLVLLLTLGSSHGTGPGMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R26954;
10-FEB-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-1992.
07-FEB-1992; F00111.
08-FEB-1991; FR-001487.
12-APR-1991; FR-004527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See 028120-028172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Mstch
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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ID W2
AC W2
DT 29
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When mammalian vesicle membrane transport protein - and corresp.

DNA, vectors, transformed cells and antibodies, for diagnosis and treatment of neurological disorders, e.g. Parkinson disease

Frample 2; Page 111-112; 181pp; English.

Example 2; Page 111-112; 181pp; English.

This sequence of the tetracypline transporter protein showed a definite homology with the chromaffin granule anine transport protein (GGAT) of rat. The CDNA encoding the chromaffin granule amine transport protein is useful in gene therapy and as a probe for detecting genomic sequences. The transport protein is used for creening cytotoxic compounds implicated in Parkinsons disease, screening cytotoxic compounds implicated in Parkinsons disease, classases associated with activity of neurotoxins or psychiatric diseases associated with activity of neurotoxins or psychiatric activate its action. Antibodies raised against the transport protein as settinity reagents for purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
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20-M06-1998 (first entry)
Mouse apoptosis inducing receptor.
Apoptosis inducing receptor; AIR protein; mouse; cell death regulator;
Type I transmembrane protein; tumour cell death; autoimmune disesse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 14.9%; Score 83; DB 1; Length 194; Local Similarity 31.0%; Pred. No. 7.29e+01; hes 18; Conservative 13; Mismatches 23; Indels 4; Gaps
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNSSTKIALVITLLDAM-GIGLIMPVLPTLLRE-FIASEDIANHFGVLLA-LYALMQV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01.001.1994 (first entry)
Peptide fragment of terracycline transporter protein.
Peptide fragment of terracycline transporter protein;
Vesicle membrane transport protein; gene therapy; screening;
Parkinsons disease; neurotoxin; identification; detection;
antibody; probe; chromaffin granule amine transporter protein;
resistance; terracycline.
Bscherichia coli.
W09325699-A.
                                                                                                                                                              3;
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                                                                                              Score 84; DB 1; Length 795;
Pred. No. 6.24e+01;
12; Mismatches 11; Indels
                                                                                                                                                                                                                       633 LGCGLPLLLTLAAYGALGRAVLRSPGMTVAEKLRVAALVASG 674
                                                                                                                                                                                                                                                               W57046 stsndard; Protein; 411 AA.
                                                                                                                                                                                                                                                                                                                                                                                     T 8
R47338 standsrd; Protein; 194 AA.
                                                                                                    Match 15.1%;
Local Similarity 38.1%;
Les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1993; U05704.
11-JUN-1992; U0-999074.
30-JUL-1992; US-999074.
(REGC.) UNIV CALIFORNIA.
Edwards RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-1998.
03-OCT-1997; U17876.
04-OCT-1996; US-044456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP.
Perkins PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 98-240077/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 AA;
                                           795 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 94-007556/01
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WO9814565-Al.
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Sequence

Query Match

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Misc_difference
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 54-55; 71pp; English.

CII-3 (W11674) comprises a subunit of complex II of the human mitochondrial electron transport chain. It is the expression product of the CII-3 gene identified in mammalian artificial chromosome MAC-8.2.3, which is contained in the human-hamster hybrid cell line XEWB.2.3 (ATCC CR. 11991). A portion of the CII-3 gene (see also T72461-65) or of CII-3 CDNA (T72466) can be utilised as a unique cloning site and selectable marker in an MAC, allowing the site-specific integration of an exogenous nucleic acid sequence into the MAC. The MAC can be used for stable expression of large fragments of DNA and also for the production of transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 7-transmendran receptor HNFDY20,
HNFDY20; G-protein coupled receptor; human; infection; HIV; Pain;
cancer; anorexia; asthma; Parkinson's disease; acute heart failure;
hypotension; hypertension; urinary retention; osteoporosis;
angina pectoris; myocardial infarction; ulcer; allergy;
benign protettic hypertrophy; psychosis; anxiety; schizophrenia;
manic depression; delirium; dementia; mental retardation;
dyskinesia; Huntingdon's disease; Gilles de la Tourette's syndrome;
therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                           New mammalian artificial chromosomes – comprising a mammalian centromere and a unique cloning site, used for stable expression of large fragments of DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucieotides and polypeptides encoding a novel human 7-transmembrane receptor - useful for diagnosing and treating e.g. cancer, osteoporosis and Parkinson's disease and infections caused by HIV-1 or -2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ciaim 1; Page 18-19; 24pp; English.
This polypeptide comprises HREDY20, a novel human 7-transmembrane of protein coupled receptor that shows about 30.8% identity in 299 amino acid residues with the thrombin receptor. Its amino acid sequence was deduced from an isolated HREDY20 polynuclectide sequence (see V35631). The invention relates to HREDY20 polypeptides and recombinant materials and methods for their production. It also provides methods for using such polypeptides and HREDY20 polypericetides for treatment of infections such as bacterial, fungal, protozoan and particularly HIV-1 or HIV-2
Mammalian artificial chromosome; MAC; selectable marker; CII-3; mitochondrial electron transport chain complex II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 SLPMAMSICHRGTGIALSAGVSL-FGMS-ALLLPGNFES-YLELVKSLCL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82; DB 1; Length 169;
Pred. No. 8.52e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-FEB-1998; 301122.
19-MAR-1997; US-820521.
(SMIK ) SMITHKLINE BEECHAM CORP.
BETGRIM D., FURCLETER WS, MAO JY, Sathe GM;
WPI: 98-482962/42.
N-PSDB; V53631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n 12
W59924 standard; Protein; 401 AA.
W59924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 14.7%;
Best Local Similarity 28.0%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-1998 (first entry)
                                                                                                                                     09-MAY-1997.
29-OCT-1996; U17476.
31-OCT-1995; US-550717.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                               WPI; 97-272103/24.
N-PSDB; T72466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 169 AA;
                                                                                                                                                                                                                                                    Scheffler IE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                  Homo sapiens
WO9716533-A1
                                                                                                                           09-MAY-1997
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      NAMES OF THE PART 
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This sequence represents the murine protein, designated misha, which may be a mammalian homologue of the Saccharomyces cerevisiae general repressor protein Sin3. The mish protein associates with a Mad be a mammalian homologue of the Saccharomyces cerevisiae general repressor protein Sin3. The mish protein associates with a Mad be polypeptide to form a mish: Mad and complex which binds to a nucleotide sequence comprising CACGTG. Mad is a basic helix-loop-helix (bHiH) zipper protein Which can compete with Myc by forming sequence. Specific DNA-binding heterocomplexes with Max. Mad.Max. contplexes repress, while Myc: Max complexes repress, while Myc: Max complexes repress, while Myc: Max complexes activite, transcription from promoters containing proximal CACGTG binding sites for these proteins. Expression of Mad is closely linked to differentation in at least two distinct call lineages. The switch from Myc: Max to Mad! Max complexes may reflect the repression of transcription of Myc regulated genes by Mad. The DNA, vectors and host contains useful in elucidation of Mad repressor functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W10038 standard; Protein; 1253 AA.
W10038;
W10038;
W10038;
W10038;
W2 core in the introduction of introduction
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                                astima, Parkinson's disease, acute heart failure, hypotension, the procession of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mSin nucleic acids encoding recombinant polypeptide(s) that associate with Mad polypeptide - are possible homologues of S. cerevisiae general repressor protein Sin3 Example 12; Fig 23A-C; Illipp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
infections, and conditions including pain, cancers, anorexia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 81; DB 1; Length 401;
Pred. No. 9.94e+01;
9; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-APR-1997.
29-APR-1997.
01-JWN-1994; 252966.
01-JWN-1994; US-222966.
19-SEP-1991; US-756195.
01-APR-1994; US-222638.
(HUTC-) HUTCHINSON CANCER RES CENT FRED.
WPI; 97-288216/23.
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/note= "encoded by TAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The main nucleic acids encoding recombinant polypeptide(s) that associate with Mad polypeptide - are possible homologues of S. cerevisiate general repressor protein Sin3 associate with Mad polypeptide - are possible homologues of S. cerevisiate general repressor protein Sin3.

Example 12: Fig 294-C; 1118p; Engqlish.

This sequence represents the murine protein, designated mSinA9, which may be a mammalian homologue of the Saccharomyces cerevisiate general repressor protein Sin3. The mSin med max complex which binds to a polypeptide to form a mSin:Mad.max complex which binds to a nucleotide sequence comprising GACGTG. Mad is a basic helix-loop-helix conclected by an expectation which can compete with Myc by forming sequence. Secure in the Myc.Max complexes repress will may mad and sequence comprising conference of the secure of the sequence of the sequence complexes activate, transcription from promoters containing closely linked to differentation in at less two distinct call lineages. The switch from Myc.Max to Mad:Max complexes may reflect the repression of transcription of Myc regulated genes by Mad. The DNA, vectors and host cells of the invention are useful for the recombinant production of mSin Squence 1261 AA;
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                                                                                                                                                                                                                                                                                                       Mad binding protein, mild.
Mad binding protein, mild.
Murine; mild.
Murine; mild.
Max. mammalian homologue; Saccharomyces cerevisiae; repressor
Sin3; Mad; Max; miln.Mad complex; mild.Max complex; Myc; promoter;
basic helix-loop-helix zipper protein; compete; DNN-binding;
Myc: Max complex; activate; transcription; gene regulation.
Mus musculus.
                                                             Gaps
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              Score 81; DB 1; Length 1253;
Pred. No. 9.94e+01;
                                                           14; Mismatches 14; Indels
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                                                                                                     949 VLGIKRDKSDSPAIQLRLKEPMDVDVEDYYPAFLDMVRSL 988
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                                                                                                                             :|| : ::||:||: | ::||::|| | 13 LLGSSHGTGPGMTLQLKLKESF-LTNSSYESSFLELLEKL 51
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R15138 standard; Protein; 398 AA.
R15138;
17-FEB-1992 (first entry)
Human serotonin 1D receptor encoded by gene 11.
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Pred. No. 9.94e+01;
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19-SEP-1991; US-756195.
23-UN-1992; US-903710.
01-APR-1994; US-222638.
(HUTC-) HUTCHINSON CANCER RES CENT FRED.
Ayer DE. Elsenman RN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- unknown
/note- "encoded by TAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lsbel= unknown /note= "encoded by
                                                                                                                                                                                                                                       W10040 standard; Protein; 1261 AA.
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Best Local Similarity 27.5%;
Matches 11; Conservative
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                                Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc_difference 1247
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01-JUN-1994; 252966.
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              Query Match
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Weinshank RL, Branchek T, Hartig PR;
West Signal Old Signal SHT-ID receptors and their antibodies -
T receptor expression e.g. dementia
S Claim 7: Fig 4; 90pp; English.
T receptor expression e.g. dementia
S Claim 7: Fig 4; 90pp; English.
T receptor expression e.g. dementia
S Claim 7: Fig 4; 90pp; English.
T receptor expression e.g. dementia
S Claim 7: Fig 4; 90pp; English.
T receptor and gene 8-30-84
C and gene 11, respectively. A full-length clone corresponding to
Gene 11 was isolated from a human placental library. The
main acid sequence deduced from the nucleotide sequence with
previously characterised neurotransmitter receptors suggests that
it is a new member of the G protein-coupled receptor family.
See Q14835 for gene 11.
Sequence 398 Ax;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l; Gaps
5-HT (1D); Parkinson's Disease; migraine; anxiety; eating disorder; G-protein; 5-hydroxytryptamine.
Romo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 14.3%; Score 80; DB 1; Length 398; Best Local Similarity 23.6%; Pred. No. 1.16e+02; Matches 17; Conservative 22; Mismatches 32; Indels
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/label= cytoplasmic_tail
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                                                                                                                                                                                                                                                                            transmembrane-2
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/label transmembrane-6
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/label- transmembrane-7
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/label- extracellular
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'label- extracellular
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Ne : 10 secs.
                                                                             Location/Qualifiers
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/label- †-
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5.5.04e+01 5.04e+01 5.04e+01 5.04e+01 5.04e+01 5.04e+01 6.09e+01 6.09

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Sequence 51, Application US/08118270
C PATENT NO. 19984
C RENERAL INFORMATION:
APPLICANT: Wurphy, Randall B.
APPLICANT: SCHORGE, DAVID II
TITLE OF INVENTION: POLYEPPIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: PECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
TORRESPONDENCE ADDRESS: 346
CORRESPONDENCE ADDRESS: 346
CONFORT: USA
COUNTY: Washington
STREE: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDR COMPATIBLE
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: D.C.
COM
                     Sequence 52, Applicati 5 sequence 52, Applicati 5 sequence 46, Applicati 5 sequence 33, Applicati 5 sequence 34, Applicati 5 sequence 2, Applicati 5 sequence 2, Applicatio 5 sequence 29, Applicatio 5 sequence 29, Applicatio 6 sequence 3, Applicatio 6 sequence 3, Applicatio 6 sequence 3, Applicatio 6 sequence 1, Applicatio 9 sequence 1, Applicatio 9 sequence 2, Applicat
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Sequence 51, Application US/08118270
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2.28e+01
2.68e+01
3.14e+01
3.14e+01
3.68e+01
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(1-78) from US09092296.pep
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1 MGSGLPLVLLTLIGSSH0T......SGTSVTLHHARSQHHVVCNT 78
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                                                                                                                                                                                                                                                                                                           Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1
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Listing first 45 summaries
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Match Length
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Gap 11
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Perfect Score:
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Matches
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GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
WUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Weahington
STATE: D.C.
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                                                                                      Query Match 15.2%; Score 85; DB 1; Length 325; Best Local Similarity 44.4%; Pred. No. 2.28e+01; Matches 12; Conservative 5; Mismatches 8; Indels
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COMPUTEY: USA
COMPUTEY: USA
COMPUTEY: E1004
COMPUTEY: INPO
COMPUTEY
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                                                                                                                                                                                                                                                                 325 AA.
                                                                                                                                                                                                                                                                 PRT;
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 325 AA; 37288 MW; 592694 CN;
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TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 325 AA; 37288 MW; 592694 CN;
                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application PC/TUS9308528
                                                                                                                                                      27 YMKLKTYASVFLLNLALADLCFLLTLP 53 :: : | | | | : | | | | | | | | 34 FLINSSYESSFL-EL-LEKICLLHLP 58
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PCT-US93-08528-51
                                                  SEQUENCE
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Sequence 2, Application US/09009438
Patent No. 5981223
GENERAL PRORMATION:
APPLICAMT: SATHE, GANESH M.
APPLICAMT: BERGSMA, DERR, J.
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: RATHER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
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                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDION TYPE: Diskette
COMPUTER: INACCOMPACTION
COMPOTER: TRM COMPACTION
SOFTWARE: EsastED for Windows Version 2.0
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,438
FLIASIFICATION:
RESPECTATION:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GH-70369
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: Protein
SEQUENCE 374 AA; 40345 MW; 690567 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNAY AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08063552
                                                                                                             Sequence 2, Application US/09009438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 610-407-0701
TELEX: 846159
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acids
STANDARD;
                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 1inear
                                                                                                                                                                                                                                                                                                                                                                                                              USA
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ID US-08-063-552-8
AC XXXXXX
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DE Sequence 8, Applic
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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STANDARD;
                                                                                                                                                                                                                         14.9%;
Local Similarity 31.0%;
les 18; Conservative
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ID US-08-741-406-2
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application PC/IUS9305704
GENERAL INFORMATION:
APPLICANT: Edwards, Robert H
TITLE OF INFORMATION:
CORRESPENDENCE 17
CORRESPENDENCE Abdors & wak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STATE: California
COUNTRY: USA
ZIP: 91001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
Patent No. 5688936
GENERAL INFORMATION:
APPLICANT: Edwards, Robert H
APPLICANT: Edwards, Robert H
TILE OF INVENTION: Vesicle Membrane Transport Proteins
NUMBER OF SCHOENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Sheldon & Mak
STREET: 225 South Lake Avenue, Ninth Floor
CITY: Pasadena
STARET: California
CONTEX: OSA
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLIA
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN
OPELICATION NUMBER: US/08/063,552
FILING DATE: 19930514
CLASSIFICATION NUMBER: US/08/063,552
FILING DATE: 19930514
CLASSIFICATION NUMBER: 930
ATTORNEY/AGERT INFORMATION:
NAME: Farber, Michael B
REGISTRATION NUMBER: 93,512
REFERENCE/DOCKET NUMBER: 9067-1
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 796-400
TELEPHONE: (818) 796-401
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: AMINO ACID
TIPELE AMINO ACID
TIPELE AMINO ACID
                                                                                                                                                                                                                                                                                                                                                         Score 83; DB 1; Length 194;
Pred. No. 3.14e+01;
13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGENT TYPE: internal
ORGINAL SOURCE:
ORGANISM: Transposon 10
JENCE 194 AA; 20868 WW; 201442 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application PC/TUS9305704
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 31.0%;
Matches 18; Conservative
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PCT-US93-05704-8
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4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08741406
Patent No. 572118
GENERAL INFORMATION:
APPLICANT: SCHEfiler, Immo E.
TITLE OF INVENTION: Membalian Artificial Chromosomes and
TITLE OF INVENTION: Methods of Using Same
NUMBER OF ENQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4470 La Jolla Village Drive, Suite 700
CITY: San Dago
STATE: California
COUNTRY: United States
ZIP: 9212
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/741,406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 83; DB 3; Length 194;
Pred. No. 3.14e+01;
13; Mismatches 23; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: PCT/US93/05704
FILING DATE: 19930611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 AA
                                                                                               FILING DATE: LOCATION CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farber, Michael B
REGISTRATION NUMBER: 32,612
REFERNICE/DOCKET NUMBER: 9067-1PCT
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 796-6321
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 anino acids
TYPE: AMINO ACID
TOPOLOGY: 11near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/550,717
FILING DATE: 31-0CT-1995
ATORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,915
REFERENCE/DOCKET NUMBER: P-UD 2317
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECCLE TYPE: peptide
HYPOTHETICAL: NO
FRAGNENT TYPE: internal
ORGANISM: Transposon 10
ORGANISM: Transposon 10
UENCE 194 AA; 20868 MW; 201442 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Gaps

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Score 81; DB 2; Length 401;
Pred. No. 4.31e+01;
9; Mismatches 4; Indels
         SQ SEQUENCE 401 AA; 44386 MW; 855771 CN;
                                                                                                                332 YFSSSGFQADFHELLRRLCGL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                         Query Match
Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                     US-08-252-966B-12
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Patent No. 5942416
GENERAL INFORMATION:
APPLICANT: Bergama, Derk
APPLICANT: Geneah, Sathe
APPLICANT: Geneah, Sathe
APPLICANT: Money
APPLICAN
                                                                                                                                                                                            Query Match 14.7%; Score 82; DB 1; Length 169; Best Local Similarity 28.0%; Pred. No. 3.68e+01; Matches 14; Conservative 20; Mismatches 13; Indels 3;
                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,521
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER::
                                                                                                                                                                                                                                                                                                                                                                               401 AA.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8001
TELEPAX: (619) 535-8049
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 169 AA; 18610 MW; 162524 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/ASENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/CDCKET NUMBER: GH50011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08820521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 401 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                         US-08-820-521-2
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Sequence 12, Application US/08252966B
Patent No. 5524818
GENERAL INFORMATION:
APPLICANT: Elsenman, Robert N.
APPLICANT: APELICANT: APELICANT: Hurlin, Peter J.
APPLICANT: APELICANT: Mad or Max
TITLE OF INVENTION: Regulatory Proteins that Dimerize with
TITLE OF INVENTION: Mad or Max
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Christensen, O'Connor, Johnson, and KindnessPLLC
SIRET: 1420 Fifth Ave., Suite 2800
CITT: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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DESCRIPTION: translation of maina cDNA; see Figure 23
DESCRIPTION: translation of maina cDNA; see Figure 23
ORIGINAL SOURCE:
ORGANISM: Mus musculus
UENCE 1253 AA; 142589 MW; 7863283 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

IIP: 99101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING STSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTER Release #1.0, Version #1.25
CURRENT APPLICATION DATE: 01-70N-1994
CLASSIFICATION NUMBER: US/08/252,966B
FILING DATE: 01-70N-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis R.
REGISTRATION NUMBER: 26,997.
REGISTRATION NUMBER: 26,997.
RESTERENCE/DOCKET NUMBER: PHORITON:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 682-8100
TELECHONE: (206) 682-8100
TELECHONE: (206) 244-0779
INFORMATION POR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
FWACTH: 1253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.5%; Score 81; DB 1; Length 1253; Best Local Similarity 27.5%; Pred. No. 4.31e+01; Matches 11; Conservative 14; Mismatches 14; Indels
                                                                                                                                                  1253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          949 VLGIKRDKSDSPAIQLRLKEPMDVDVEDYYPAFLDMVRSL 988
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                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08252966B
                                                                                                                                               STANDARD;
34 FLINSSYESSFLELLEKICLL 54
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PRT;
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                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 30.8%;
Matches 16; Conservative
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 11
US-08-117-006-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein DESCRIPTION: translation of msina9 cDNA; see Figure 29A, B, C, D HYPOTHETICAL: YES
                                                                                                                                                                                            COUNTRY: Seattle
STREET: 1420 Fifth Ave., Suite 2800
CITY: Seattle
STREET: 1420 Fifth Ave., Suite 2800
CUNTRY: USA
LIF: 98101-2347
COMPUTER: PEPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/252,966B
FILING DATE: 01-UN-1994
CITASSIFICATION NUMBER: 26,997.
REFERENCE/DOCKET NUMBER: 26,997.
REFERENCE/DOCKET NUMBER: 26,997.
REFERENCE/DOCKET NUMBER: 26,997.
REFERENCE/DOCKET NUMBER: 26,997.
TELEFONIC CHARACTERISTICS:
LENGTH: 1261 amino acids
TYPE: STORMENTERNEENTERS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                           Sequence 18, Application US/08252966B
Patent No. 5624818
GENERAL INFORMATION:
APPLICANT: Bisenman, Robert N.
APPLICANT: Hurlin, Peter J.
APPLICANT: Hurlin, Peter J.
APPLICANT: Hurlin, Peter J.
APPLICANT: Ayer, Donald E.
TITLE OF INVENTION: Regulatory Proteins that Dimerize with NUMBER OF SUDGENERS: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 14.5%; Score 81; DB 1; Length 1261;
Best Local Similarity 27.5%; Pred. No. 4.31e+01;
Matches 11; Conservative 14; Mismatches 14; Indels
                 1261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    949 VLGIKRDKSDSPAIQLRLKEPMDVDVEDYYPAFLDMVRSL 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
NCE 1261 AA; 143711 MW; 7937040 CN;
                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                          Sequence 18, Application US/08252966B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08828832
                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
     RESULT 9
ID US-08-252-966B-18
XX
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US-08-828-832-4
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                                     XXXXX
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Gaps
Sequence 4, Application US/08828832
Patent No. 5827711
GENERAL INFORMATION:
APPLICANT: Dal, Freet,
APPLICANT: Shah, Purvi
TILLE OF INVENTION: NOVEL SUCCINATE DEHYDROGENASE SUBUNIT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STRET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READMALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: EMA Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastECD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
ELING DATE: Herewith
CLASSIFICATION: 435
FRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08117006
Patent No. 5639652
GENERAL INFORMATION:
APPLICANT: Welnshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Branchek, Theresa
APPLICANT: BRANCHIG, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HIIF RECEPTOR AND TITLE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80; DB 2; Length 169;
Pred. No. 5.04e+01;
18; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET WUBER: PF-0250 US
TELECOMMUNICATION:
TELECHONE: 415-855-0555
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US-08-216-594-6
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    88888888888888888888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application PC/TUS9300149
GENERAL INFORMATION:
APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
IITLE OF INVENTION: DNA ENCODING A HUMAN 5-HILF RECEPTOR AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Cooper 6 Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 14.3%; Score 80; DB 1; Length 390; Local Similarity 23.6%; Pred. No. 5.04e+01; nes 17; Conservative 22; Mismatches 32; Indels 1; Gaps
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CLASSIFICATION: 514

ATORNEY/AGENT INFORMATION:

RAME: White, John P
REGISTRATION UNMERS: 28,678

REFERENCE/DOCKET NUMBER: 1795/39318

TELECOMMUNICATION INFORMATION:
TELEPRONE: 212-977-9550

TELEFAM: 212-664-0525

TELEFAM: 212-664-0525

TELEFAM: 390 annio acids
TYPE: annio acid
STRANDEDNESS: unknown
TYPE: annio acid
STRANDEDNESS: unknown
TOROCXY: linear
MOLECULE TYPE: protein
                                                                                    ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect, Version 5.1
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/08/117,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
IMMEDIATE SOUNCE:
CLONE: 5-FILDB
SEQUENCE 390 AA; 43656 MW; 849817 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application PC/TUS9300149
  ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
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                                  New York
: New York
RY: USA
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66 HHARSQHHVVCN 77
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PCT-US93-00149-6
                                                                         COUNTRY:
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COMPTER: TARROW COMPANDED FOR AND COMPANDED STREET, CLOOPED AND COMPANDED STREET, CLOOPED AND COMPANDED AND COMP
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Sequence 6, Application US/08542358

Patent No. 5786155

CENERAL INFORMATION:
APPLICANT: Wealshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Branchek, Theresa
TITLE OF INVENTION: DAB ENCODING A HUMAN 5-HTIE RECEPTOR AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham LLP
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham LLP
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Cooper & Dunham LLP
CORRESPONDENCE ADDRESS:
CONTREST: New York
COUNTRY: U.S.A.
CLIY: 10036
COMPUTER READABLE FORM:
COMPUTER: EDRPY disk
COMPUTER: EDR PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/542,358
                                                                                                                                                                                                                                                                                                                                                                                                                           52 LVMLLALITLATILSNAFVIATVYRTRKLHIPANYLIASLDVTDLLVSILVIPISTMYTV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.3%; Score 80; DB 1; Length 390;
Best Local Similarity 23.6%; Pred. No. 5.04e+01;
Matches 17; Conservative 22; Mismatches 32; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 AA.
                 FILING DATE: 19920108
CLASSIFICATION: 514
ATTONIEVAGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERRINGE/DOCKET NUMBER: 1795/39318
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFX: 212-977-9550
TELEX: 42253 CDOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CLARACTERISTICS:
LENGTH: 390 maino acids
TYPE: AATNO ACID
STRANDENDESS: unknown
                                                                                                                                                                                                                                                                                                                          E: 5-HILDB
390 AA; 43656 MW; 849817 CN;
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-terminal IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
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CLASSIFICATION: 435
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US-08-542-358-6
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SEQUENCE 3
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Patent No. 5360735
GENERAL INFORMATION:
APPLICANT: Weinshank, Richard L
APPLICANT: Branchek, Theresa
APPLICANT: Bartig, Paul R
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper 6 Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 LVMLLALITLATILSNAFVIATVYRTRKLHTPANYLIASLDVTDLLVSILVIPISTMYTV 111
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURREY APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/216,594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P REGISTRATION NUMBER: 1795/39318
REFERENCE/DOCKET NUMBER: 1795/39318
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-977-9550
TELEFAX: 212-64-0525
TELEFAX: 42253 CDOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acids
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: nuclean
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
INMEDIATE SOURCE:
CLONE: 5-HT1DB
SEDUENCE
CLONE: 5-HT1DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New YORK
STATE: New YORK
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAYR:
APPLICATION NUMBER: US/07/817,920
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CC TELECOMMUNICATION INFORMATION:
CC TELECOMMUNICATION INFORMATION:
CC TELECHAR: 212-391-0525
CC TELEPAX: 212-391-0525
CC TELEPAX: 212-391-0525
CC TELEPAX: 212-391-0525
CC SEQUENCE CHRARACTERISTICS:
CC SEQUENCE CHRARACTERISTICS:
CC TYPE: amino acid
CC TYPE: amino acid
CC TYPE: amino acid
CC TYPE: protein
CC TYPE: protein
CC TYPE: Drotein
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Mar 20 12:32:21 2000; MasPar time 8.96 Seconds 410.868 Million cell updates/sec Tabular output not generated. Run on:

>US-09-092-296-15 (1-78) from US03092296.pep 558 1 MGSGLPLVLLITLGSSHGT......SGTSVTLHHARSQHHVVCNT 78 Description: Perfect Score: Sequence: Title:

PAM 150 Gap 11

Scoring table:

142080 segs, 47172406 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir62 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 39.408; Variance 84.670; scale 0.465 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	8.92e-02	9.25e-01	1.23e+00	1.63e+00	2.85e+00	2.85e+00	3.76e+00	3.76e+00	4.95e+00	4.95e+00	6.50e+00	8.53e+00	1.11e+01	1.11e+01	1.11e+01	1.45e + 01	1.45e + 01	1.45e + 01	1.45e + 01	1.45e+01	1.89e+01	1.89e+01	1.89e + 01
Description	protein export membra	ubiquinolcytochrome	translation requlator	osmotin-like protein	hypothetical protein	homeotic protein zfh-	daunorubicin resistan	K12H4.8 protein - Cae	hypothetical protein	probable translation	flagellar motor appar	hypothetical protein	dihydroorotase (EC 3.	probable tyrosine kin	hypothetical protein	hypothetical protein		tetracycline resistan	hypothetical protein	beta-galactosidase (E	mitotic-specific cycl	T-cell receptor alpha	T-cell receptor alpha
Ω	C70384	863638	A48156	JC5237	S73757	533642	B75076	S44849	S43071	S58161	S39641	H64082	S74800	T03130	S76731	D70324	T14243	YTECTO	G65058	A37086	\$53000	\$22896	\$23368
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Query Match	18.1	16.7	16.5	16.3	15.9	15.9	15.8	15.8	15.6	15.6	15.4	15.2	15.1	15.1	15.1	14.9	14.9	14.9	14.9	14.9	14.7	14.7	14.7
Score	101	93	92	91	89	8	88	88	87	87	86	85	84	84	84	83	83	83	83	83	82	82	82
Result No.	-	7	9	4	S	·φ	7	œ	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23

\$63638 *type complete
ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b
- Allomyces macrogynus mitochondrion
apocytochrome b
#formal_name mitochondrion Allomyces macrogynus
28-oct-1996 #sequence_revision 27-Feb-1997 #text_change
20-sep-1999
\$63635

ALTERNATE_NAMES ORGANISM DATE

ACCESS IONS REFERENCE

1.89e+01 1.89e+01 1.89e+01 1.89e+01 1.89e+01 1.89e+01 2.46e+01 2.46e+01 2.46e+01 2.46e+01 2.46e+01 2.46e+01 2.46e+01 2.46e+01 2.46e+01 2.46e+01 3.46e+01 3.19e+01 3.19e+01	
T-cell antigen recept invasion protein invE NADH dehydrogenase su ent-Kaurene synthase polyprotein - fava be moch protein - recept g protein-coupled rec g protein-coupled rec g protein-coupled rec g protein-coupled rec g protein receptable chart 3 protein probable next3 protein hypothetical protein co-repressor protein hypothetical protein	
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ALIGNMENTS

c70384 *type complete protein export membrane protein SecD - Aquifex aeolicus *formal_name Aquifex aeolicus 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 10-Sep-1999 C70384 A70300 Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,	Na There of C7 C7 C7 C7 C7 C8 E8 F8 #8	Query Match 18.1%; Score 101; DB 1; Length 501; Best Local Similarity 38.3%; Pred. No. 8.92e-02; Matches 18; Conservative 10; Mismatches 18; Indels 1; Gaps 1; Matches 18; Conservative 10; Mismatches 18; Indels 1; Gaps 1; Matches 18; Lill 1 1 1 1 1 1 1 1 1 1
RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors	#journal #title #cross-refe #accession ##molecu ##molecu ##cross-	Query Mat Best Loca Matches Db 454 v Qy 8 v RESULT 2 ENTRY

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#domain cytochrome b homology #label CBH\
#domain cytochrome b6 homology #label CB6\
#domain plastoquinol--plastocyanin reductase 17k protein
homology #label 17k\
#binding_site heme iron, low potential (His) (axial
ligands) #status predicted\
#binding_site heme iron, high potential (His) (axial
ligands) #status predicted
#blength 382 #molecular-weight 43467 #checksum 6973
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##molecule_type DNA
##residues 1-712 ##label OLI
##cross-references EMEL:268195, NID:91122341; PID:e213795; PID:91122344;
##cross-references EMEL:268195, NID:91122341; PID:e213795; PID:91122344;
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                                                                                                                                                                                                                                                                                                                                                                                                          67/3: 137/3: 143/3: 164/1: 200/2: 252/3

#superfamily cytochrome b; cytochrome b homology; cytochrome bb fmonlogy; plastoquinol--plastocyanin reductase 17R
protein homology electron transfer; heme: iron; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain
  #authors Paquin, B.; Lang, B.F.
#journal J. Mol. Biol. (1996) 255:688-701
#title The mitochondrial DNA of Allomyces macrogynus: the complete genomic sequence from an ancestral fungus.
#cross-references MUID:96226032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ë,
                                                                                                                                                                                                                                                                                     the nucleotide sequence was submitted to the EMBL Data
Library, November 1995
                                                                                                                                                       nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Bushman, J.L.; Asuru, A.I.; Matts, R.L.; Hinnebusch, A.G. #journal Mol. Cell. Biol. (1993) 13:1920-1932
#title Evidence that GCD6 and GCD7, translational regulators of GCN4, are subunits of the guanine nucleotide exchange factor for eIF-2 in Saccharomyces cerevisiae.
#accession A48156
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##residues
##cross-references EMBL:L07115; NID:g171572; PID:g171574
##ctoss-reference extracted from NCBI backbone (NCBIN:126018,
                                                                                                                                                          ##status
##molecule_type DNA
##crosduces 1-382 ##label PAQ
##crosd-references EMBL:U41288; NID:91236403; PIDN:AAC49221.1;
##crosd-references EMBL:U4128404
PID:91236404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 93; DB 2; Length 382;
Pred. No. 9.25e-01;
15; Mismatches 16; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S61576 "CALTIS, D. Oliver, K.; Harris, D. Submitted to the EMBL Data Library, December 1995 S61578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 PGWILQLK-LKESFL-TNSSYESSFLELLEKLCLLLHLPSGTSVTLHHARS 70
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Best Local Similarity 33.3%;
Matches 17; Conservative
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#submission
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CLASSIFICATION
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#authors
#journal
#title
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10-210
222-340
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#gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
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5/3757 #type complete
hypothetical protein Fil_orf879 - Mycoplasma pneumoniae (ATCC 29342) (SGC3)
#formal_me Mycoplasma pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Chen, R.; Wang, F.; Smith, A.G.
#fournal Gene (1996) 179:301-302
#title A flower-specific gene encoding an osmotin-like protein from Iycopersicon esculentum.
#cross-references MUID:97128324
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#product osmotin-like protein #status predicted #label
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Cosmotin-like protein precursor - tomato
#formal_name lycopersicon esculentum #common_name tomato
13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change
JC5237
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#length 252 #molecular-weight 27265 #checksum 2939
                                                                                          translation regulation
#length 712 #molecular-weight 81160 #checksum 142
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#residues 1-252 ##label CHE
##cross-references GB.L76532; NID:91220536; PID:91220537
COMMENT This protein is rich in cysteine content and play a
flowers defense mechanisms against pathogens.
CLASSIFICATION #superfamily thaumatin I
                                                                                                                                                   Score 92; DB 2; Length 712;
Pred. No. 1.23e+00;
8; Mismatches 14; Indels
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Pred. No. 1.63e+00;
4; Mismatches 7; Indels
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#title Complete sequence analysis of the genome Mycoplasma pneumoniae.
                                                                                                                                                                                                                              12 IGN-HGKNSDMDVEDRLQAVVLTDS-YETRFMPLTAVKPRCLL 52
                                                                                                                                                                                                                                                   ##cross-references SGD:S0002619; MIPS:YDR211w
##experimental_source strain AB972
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Best Local Similarity 39.5%;
Matches 17; Conservative
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Best Local Similarity 54.2%;
Matches 13; Conservative
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33-496
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FRICATION #superfamily unassigned homeobox proteins; homeobox homology
NDS DNA biding: homeobox; nucleus; transcription regulation;
zinc finger
                                                                                                                                                                                                                                                                                                                                       $33642 *type complete homeoric protein 2fh.2 - fruit fly (Drosophila melanogaster) *formal_name Drosophila melanogaster 20.Feb-1995 *sequence_revision 20-Feb-1995 *text_change
##molecule_type DNA
##residues
1-879 ##label HIM
##cross-references EMBL:AED0042; GB:U00089; NID:g1674112; PID:g1674117
##note the nucleotide sequence was submitted to the EMBL Data
Library, November 1996
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#journal Mech. Dev. (1991) 34:113-122
#title The Drosophila 2fh-1 and 2fh-2 genes encode novel proteins
containing both zinc-finger and homeodomain motifs.
#cross-references MulD:92001539
#accession S33642
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20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
20-Aug-1999
875076
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#domain homeobox homology #label HOX2\
#domain homeobox homology #label HOX3
#domain homeobox homology #label HOX3
#length 3005 #molecular-weight 332056 #checksum 7516
                                                                                                                             #length 879 #molecular-weight 101086 #checksum 8208
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##cross-references EMBL:M63450; NID:g158822; PIDN:AAA29051.1;
##cross-references PID:g158823
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Pred. No. 2.85e+00;
11; Mismatches 17; Indels 3;
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Pred. No. 2.85e+00;
15; Mismatches 11; Indels
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Best Local Similarity 38.0%;
Matches 19; Conservative
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S33642; S27817
S33641
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Best Local Similarity 28.9%;
Matches 11; Conservative
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17/3; 72/1; 116/3; 170/1; 216/3; 340/3; 401/3; 444/3; 512/2; 634/3; 694/3; 745/1; 855/2; 1053/1; 1113/3; 1215/3; 1321/1; 1396/2; 1458/3; 1507/3; 1563/2; 1645/3; 1677/3; 1804/2 #superfamily unassigned DEAD/H box helicases; DEAD/H box helicase ATP; P-loop
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# Berneman, Z.; Frenkel, N.; Rosenthal, L.J.
# Journal Oncogene (1994) 9:1167-1175
# Litle A transforming fragment within the direct repeat region of human herpesvirus type 6 that transactivates HIV-1.
# accession $43071
                                                                                                                                                                                                                                                                                                                                                                                                                                               844849 *type complete
K12M4.8 protein - Caenorhabditis elegans
#formal_name Caenorhabditis elegans
#formal_name Caenorhabditis elegans
14.5ep-1994 #sequence_revision 12.May-1995 #text_change
20.5ep-1999
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hypothetical protein 5 - human herpesvirus 6
#formal_name human herpesvirus 6
#formal_name kuman herpesvirus 6
19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change
17-Mar-1999
843071
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#region nucleotide-binding motif A (P-loop)/
#region nucleotide-binding motif B/
#region DEXH motif;
#region DEXH motif;
                                                                                                                             #length 314 #molecular-weight 35594 #checksum 3877
##cross_references GB:AJ248286; GB:AL096836; NID:g5458366; PID:el515808; PID:g5458423 ##experimental_source strain Orsay
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31.4%; Pred. No. 3.76e+00;
ative 17; Mismatches 15; Indels 3;
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Pred. No. 3.76e+00;
11; Mismatches 5; Indels
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##residues
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Matches 16; Conservative
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Best Local Similarity 33.3%;
Matches 8; Conservative
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                                                       **Miolecule_Type DNA
**Testidues 1-143 **Label THO
**Ercoss-references EMBL:X73675; NID:g469952; PID:g469957
**Miole the nucleotide sequence was submitted to the EMBL Data
**Library, June 1993
Y #length 143 **Molecular-weight 13317 **checksum 6533
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S58161 #type complete
probable translation releasing factor RF-1 - fission yeast
(Schizosaccharomyces pombe)
SPAC2F7.17 protein
#formal_name Schizosaccharomyces pombe
13.Jan-1996 #sequence_revision 01-Mar-1996 #text_change
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Identification of genes involved in utilization of acetate and acetoin in Bacillus subtilis.
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#superfamily translation releasing factor
#length 396 #molecular-weight 44954 #checksum 9362
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submitted to the EMBL Data Library, July 1995
S58161
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Best Local Similarity 47.2%; Pred. No. 4.95e+00;
Matches 17; Conservative 4; Mismatches 14; Indels
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15.6%; Score 87; DB 2; Length 396;
Best Local Similarity 45.0%; Pred. No. 4.95e+00;
Matches 9; Conservative 8; Mismatches 3; Indels
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Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.; Farlich, S.D.; Emmerson, P.I.; Entlan, K.D.; Errington, J.; Farlich, S.D.; Errington, P.I.; Farlich, R.D.; Errington, J.; Fagnet, C.; Farlich, M.; Fullar, Y.; Furma, S.; Galizzi, A.; Galizzi, C.; Fullar, S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandl. G.; Guy, B.J.; Haga K.; Halcch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Mananch, Rasahara, Y.; Klaerr Blanchard, M.; Klein, C.; Kobayashi, Y.; Klaerr Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningstein, G.; Kroph, S.; Kumano, M.; Murita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Mazarevto, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Marueel, C.; Medique, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Mosetl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porteetelle, D.; Porwollk, S.; Prescott, A.M.; Prescon, E.; Puljc, P.; Purnelle, B.; Rapoport, G. Rey, M.; Rospolds, S.; Rieger, M.; Rivoltk, C.; Rocha, E.; Roch, M.; Sadale, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Stol, E.; Schleich, S.; Schroeter, R.; Stol, T.; Scanlon, E.; Schleich, S.; Takeuchl, M.; Tamakoshi, A.; Tanaka, T.; Takenshi, H.; Tarkensul, M.; Tamakoshi, A.; Tanaka, T.; Takensul, M.; Vannel, M.; Vandenbol, M.; Vanneler, E.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Winters, P.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Winters, P.; Wedler, E.; Wedler, H.; Weitzenegger, T.; Winters, P.; Weller, A.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zunstein, E.; Wature (1997) 390:249-256
The complete genome sequence of the Gram-positive bacterium Bacillus subalanza
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Kikness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
FitzRugh, W.; Fleids, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, J.F.; Phillips, C.A.; Spriggs, T.; Hedellom, E., Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
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18 Aug 1995 #sequence_revision 18 Aug-1995 #text_change
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PIDN:CAB14951.1; PID:el185846; PID:92635457
##experimental_source strain 168
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#superfamily flagellar motor rotation protein
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##csidues 1-441 ##label RAN
##cross-references EMBL.D90901; GB.AB001339; NID:g1651897; PID:d1017684;
##cross-references EMBL.D905025
##note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996
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*superfamily Bacillus dihydroorotase; Bacillus dihydroorotase
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#length 441 #molecular-weight 48174 #checksum 3200
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Pred. No. 1.11e+01;
16; Mismatches 15; Indels
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                                                                                                                                                                                                                 Score 85; DB 2; Length 315;
Pred. No. 8.53e+00;
18; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                        9 TALSLSLLLSSIASAEELSAKQSLD-KMTQA-LDNLNYEIAFVQ 50
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PCC 6803
                                                                               *cross-references MUID:95350630 *accession H64082
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Best Local Similarity 32.7%;
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Best Local Similarity 29.5%;
Matches 13; Conservative
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##cross-references EMBL:D90916; GB:AB001339; NID:g1653715; PID:d1019376;
##cross-references EMBL:D90916; GB:AB001339; NID:g1653715; PID:d1019376;
##note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996

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##nolecular-weight 56720 #checksum 9647
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Rakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Simpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Tasuda, M.; Tabata, S.
#journal DNA Res. (1996) 3:109-136
#title cyanobacterium Synechocystis sp. PCC6603. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
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Baser, A.; Pflanz, R.; Fleckenstein, B.

#journal J. Virol. (1997) 71:6517-6525

#fille Primary structure of the alcelaphine herpesvirus 1 genome.

#cross-references MUDIS:97404659

#accession T03130
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probable tyrosine kinase - alcelaphine herpesvirus l
#formal_name alcelaphine herpesvirus 1
24.Mar-1999 #sequence_revision 24.Mar-1999 #text_change
07.May-1999
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Pred. No. 1.11e+01;
11; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: Mon Mar 20 12:32:35 2000 Job time: 14 secs.
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Best Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 38.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
##residues 1-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S76731
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US-09-092-296-15.rsp

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protein - protein database search, using Smith-Waterman algorithm

MPsrch_pp

Mon Mar 20 12:31:17 2000; MasPar time 5.65 Seconds 412.201 Million cell updates/sec

Tabular output not generated.

>US-09-092-296-15 (1-78) from USO9092296.pep 558 1 MGSGLPLVLLTLLGSSHOT......SGTSVTLHHARSQHHVVCNT 78 Description: Perfect Score:

Scoring table: Sequence:

PAM 150 Gap 11

82229 seqs, 29864866 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot38 1:swissprot Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 40.128; Variance 78.050; scale 0.514

Statistics:

SUMMARIES

Pred. No.	2.16e-02	3.73e-01	5.07e-01	9.30e-01	1.26e+00	1.69e+00	2.27e+00	3.04e+00	4.07e+00	5.43e+00	5.43e+00	5.43e+00	5.43e+00	7.22e+00	7.22e+00	7.22e+00	9.58e+00	9.58e+00	9.58e+00	9.58e+00	9.58e+00	9.58e+00	9.58e+00
Description	PROTEIN-EXPORT MEMBRAN	TRANSLATION INITIATION	OSMOTIN-LIKE PROTEIN P	ZINC-FINGER PROTEIN 2	HYPOTHETICAL HELICASE	PUTATIVE MITOCHONDRIAL	HYPOTHETICAL 30.1 KD P	SIGMA-E FACTOR REGULAT	HYPOTHETICAL 21.1 KD P	TETRACYCLINE RESISTANC	HYPOTHETICAL METABOLIT	BETA-GALACTOSIDASE PRE	GLUTAMATE [NMDA] RECEP	SUCCINATE DEHYDROGENAS	INVASION PROTEIN INVE.	CYTOCHROME B.	CHEMOTAXIS MOTA PROTEI	ACROSOMAL PROTEIN SP-1	PUTATIVE G PROTEIN-COU	PUTATIVE G PROTEIN-COU	CYTOCHROME B.	CYTOCHROME B.	LIPOPOLYSACCHARIDE-BIN
e e	SECD_AQUAE	E2BE_YEAST	OLP1_LYCES	ZFH2_DROME	YM68_CAEEL	RF1M_SCHPO	YTXD_BACSU	RSEB_HAEIN	YDB3_SCHPO	TCR2_ECOLI	YGCS_ECOLI	BGAL_MOUSE	NME3_HUMAN	C560_HUMAN	INVE_SALTY	CYB_ASPNG	MOTA_RHOSH	ASPX_MOUSE	GP41_HUMAN	GP42_HUMAN	CYB_SARGL	CYB_PODAN	LBP_RABIT
89	н	-	-	.	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Н	-	-
% Query Match Length	501	712	252	3005	1822	396	272	315	191	401	445	647	1233	169	372	385	253	261	346	346	386	387	482
% Query Match	18.1	16.5	16.3	15.9	15.8	15.6	15.4	15.2	15.1	14.9	14.9	14.9	14.9	14.7	14.7	14.7	14.5	14.5	14.5	14.5	14.5	14.5	14.5
Score	101	92	91	89	88	87	98	82	84	83	83	83	83	82	82	82	81	81	81	81	81	81	81
Result No.	7	7	m	4	'n	9	7	œ	6	10	11	12	13	14	12	16	17	18	19	20	21	22	23

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Gaps 1;

Score 101; DB 1; Length 501; Pred. No. 2.16e-02; 10; Mismatches 18; Indels

/ Match 18.1%; Local Similarity 38.3%; hes 18; Conservative

Query Match Best Local Si Matches 18

9.58e+00 1.27e+01 1.27e+01 1.27e+01 1.27e+01 1.27e+01 1.27e+01 1.27e+01 1.6	2.20e+01
TANA CCO CCO CCO GLU GLU AIN AIN AIN AIN AVIN WYIN CEPTO EPTO EPTO EPTO FROT	HIPOTHETICAL 29.3 AD P GLUTAMATE [NMDA] RECEP
BACA_BACLI CS60_BOVIN CYB_EMENI TCRB_PASMU OPDE_PSEAN CODT_BACSP CODT_BACSP TFI1_HUMAN ATP6_YEAST TFI1_YEAST ACHE_MOUSE A	YTXD_BACME NME3_MOUSE
5255 169 189 387 402 402 403 413 772 259 393 408 413 408 408 408 408 408 408 408 408 408 408	267 1239
44444444444444444444444444444444444444	14.0 14.0
88888888888888888888888888888888888888	78
4889001000000004444	4 4 5

ALIGNMENTS

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(BY SIMILARITY).

-!-SUBCELULIAR LOCATION: INTEGRAL MEMBRANE PROIEIN (BY SIMILARITY).

-!-SUBCELULIAR LOCATION: INTEGRAL MEMBRANE PROIEIN (BY SIMILARITY).

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                                                                                                                                                                                                             STRAIN-VF5;
MEDLINE; 98196666.
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                  NATURE 392:353-358(1998).
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT (BY SIMILARITY).
-!- SUBUNIT: PART OF THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS
WHICH COMPRISE SECA, SECB, SECE, SECE, SECE, SECG AND SECY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000716; AAC07060.1; -.
Protein transport; Translocation; Transmembrane; Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 29 POTENTIAL.

339 359 POTENTIAL.

37 391 POTENTIAL.

34 414 POTENTIAL.

470 490 POTENTIAL.

501 AA; 55459 MW; E67F690C CRC32;
                                              15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last sequence update)
PROTEIN-EXPORT MEMBRANE PROTEIN SECD.
AGLISA aeollous.
Bacteria; Aquificales; Aquificaceae; Aquifex.
               501 AA
               PRT;
               STANDARD;
                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
               SECD_AQUAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bykaryots; Metazoa; Arthropoda; Tracheta; Hexapoda; Insecta;
Pterygota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-i- IISSUE SPECIFICITY: LARGELY RESTRICTED TO THE CNS OF LATE EMBRYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 25-33.
ROBERTSON D., MITCHELL G.P., GILROX J.S., GERRISH C., BOLWELL G.P.,
SLABAS A.R.;
                                                                                                                    Lycoperalcon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: INVOLVED IN THE DEVELOPMENT OF THE EMBRYONIC CENTRAL NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                        SITALATORY 9712834.
CHEN R., WANG F., SMITH A.G.;
A flower-specific gene encoding an osmotin-like protein from
Lycopersicon esculantum.";
Gene 179:301-302(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORTHIN M.E., LAI Z., RUBIN G.M.;

"The Drosophila zfh-1 and zfh-2 genes encode novel proteins containing both zinc-finger and homeodomain motifs.";

Mech. Dev. 34:113-122(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
21-0CT-1994 (Rel. 30, Last annotation update)
21NC-FINGER PROTEIN 2 (ZINC-FINGER HOMEODOMAIN PROTEIN 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 91; DB 1; Length 252;
Pred. No. 5.07e-01;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (JAN-1997) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSMOTIN-LIKE PROTEIN.
229EB542 CRC32;
01-NGV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
OSMOTIN-LIKE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3005 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LPLSLLFTLLSLSQSTNPNFILTL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO(316; THAUMATIN; 1. PFAM; PF00314; thaumatin; 1. Cell wall; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN 25 252 O
SEQUENCE 252 AA; 27265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L76632; AAB41124.1; -. HSSP; P25871; 1AUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 th 16.3%;
Similarity 54.2%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 92001539.
                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. VF36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZFH2_DROME
P28167:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                  Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT TAKEN TO THE PROPERTY OF THE PROPERTY O
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: SUBMIT OF THE GUANNIE NUCLEOTIDE EXCHANGE FACTOR FOR EIF-2. REQUIRED TO REPRESS GGN4 TRANSLATION UNDER NONSTARVATION CONDITIONS. GCD6 AND GCD7 REPRESS GGN4 EXPRESSION AT THE TRANSLATIONAL LEVEL BY ENSURING THAT RIBOSOMES WHICH HAVE TRANSLATED UORFI WILL REINITIATE AT UORF2, -3, OR -4 AND THUS TO REACH THE GGN4 START SITE.
-- SUBMINIT: COMPLEX OF FIVE DIFFERENT SUBMITS; ALPHA (GGN3), BETA (GGD7), GAMMA (GGD1), DELTA (GGD2) AND RESILON (GGD6).
-- SIMILARIY: BELONGS TO THE EIF-28 GAMMA/FERILON SUBMITS FAMILY.
                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOT-1997 (Rel. 35, Last annotation update)
TRANSLATION INTIINION FACTOR EIF-2B EPSILON SUBUNIT (EIF-2B GDP-GTP EXCHANGE PACTOR) (GUANINE NUCLEOTIDE EXCHANGE FACTOR SUBUNIT GCD6)
GCDG OR LIF255 OR VERALIW OR YEB142.12 OR YDB142B.03.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
BUDDLINE; 9180641.
BUSHWAN J.L., ADATTS R.L., HINNEBUSCH A.G.;
EVIdence that GCD6 and GCD7, translational regulators of GCN4, subunits of the guanine nucleotide exchange factor for eIF-2 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEGUENCE FROM N.A.
STRAIN-S288C / AB972;
OLIVER K., SHORE L., HARRIS D., BARRELL B.G., RAJANDREAM M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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larity 39.5%; Pred. No. 3.73e-01;
Conservative 8; Mismatches 14; Indels
                454 VILFQF-GSGPVKGFATTLALGTIASFISNVYYAKVFLDLLNSLKIL 499
                                                     EMBL; L07115; AAA65498.1; --
EMBL; Z68194; CAA92354.1; --
EMBL; Z68195; CAA92362.1; --
PIR; Z30776; S30776.
PIR; A48156; A48156.
SGD; L0000674; GCD6.
PFAM; PF00132; havepep; 3.
Amino-acid biosynthesis; Translation regulation.
SEQUENCE 712 AA; 81161 MW; 5DAD189F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 LGN-HGKNSDMDVEDRLQAVVLIDS-YETRFMPLTAVKPRCLL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              712 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae.";
Mol. Cell. Biol. 13:1920-1932(1993)
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                     T 2
E2BE_XEAST
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ID OLP1_LYCES
AC Q41350;
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SO THE PROPERTY OF THE PROPERT

Query Match Matches

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Gaps

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EMBL; Z50142; CAA90504.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                RF1M_SCHPO
Q09691;
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                 NP_BIND
SITE
                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on lus use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcc./or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILEDON R., AINSCHOGH R., ANDERSON K., BAYNES C., BERKS M., WILEDON R., BURTDN J., CONNELL M., COPSET T., COOPER J., COLLSON A., CRAXTON M., DEAR S., DU Z., DURRIN R., FAVELLO A., FRASER A., FULTON L., GARDNER A., GREEN F. HAWKINS T., HILLIER L., JIER M., JUHNSTDN L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                       PPRM; PF00046; homeobox; 3.
PFAM; PF00066; zf-C212; 12.
Alor-finger; Metal-binding; NA-binding; Homeobox; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 9.30e-01;
11; Mismatches 17; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2165 QIKVLQEFFENNSYPKDSDLEYLSKL-LLLS-PRVIVVWFQNARQKQRKI 2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 3005;
                                                                                                                                                                                                                                    C242-TYPE.
C242-TYPE.
C242-TYPE.
C242-TYPE.
C242-TYPE.
C242-TYPE.
C242-TYPE.
C242-TYPE.
                                                                                                                                                                                                                                                                                                                                        (DEGENERATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-ROV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL HELICASE K12H4.8 IN CHROMDSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                      8B4CC45F CRC32;
SIMILARITY: CDNTAINS THREE HOMEOBDX DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1822 AA.
                                                                                                                                                                                                                                                                                                                             C2H2-TYPE.
C2H2-TYPE (1
C2H2-TYPE.
C2H2-TYPE.
HDMEOBOX 1.
HDMEDBDX 2.
                                                                                                                                                                                                                                                                                                                                                                                                   C2H2-TYPE.
                                                                                                                                                       PROSITE; PSG0027; HDMEDBDX_1; 2.
PROSITE; PSG0028; ZINC_FINGER_C2H2; 8.
PROSITE; PSG0071; HDWEOBDX_2; 3.
                                                                                                                                                                                                                              C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89;
                                                                                                                                                                                                                                                                                                                                                                                                                     3005 AA; 332056 MW;
                                                                                                EMBL; M63450; AAA29051.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        15.9%;
                                                                                                                           HSSP; P15822; 4ZNF.
TRANSFAC; T00920; -.
FLYBASE; FBGN0004607; zfh2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 38.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                 1535
11535
11856
22213
23256
23393
                                                                                                          PIR; S27817; S27817.
PIR; S33642; S33642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTDL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                               1513
1541
1797
2154
2234
                                                                                                                                                                                                                                                                                                                   1341
1438
1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P34529;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 5
YM68_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           ZN_FING
DNA_BIND
                                                                                                                                                                                                                   Repeat.
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ZN_FING
ZN_FING
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GENTLES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMLITES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMLITES (JUL.1995) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE PRDKARYCTIC AND MITOCHONDRIAL RELEASE
FACTDRS FAMILY: STRDNG, TO YEAST MRP-1.
LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M., STANDARSDNS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHDWNKEEN R., SIMS, M., SMALDON N., SHITH A., SINNIHAMER E., STADEN R., SULSTDN J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSDN R., WATENNAN R., WALLDMAN P., HALDMAN P.;

12.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00271; helicase_C; 1.
PFAM; PF00656; Ribonuclease_3; 2.
Hypothetical protein; Helicase; ATP-binding; Hydrolase; Nuclease; Endonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 88; DB 1; Length 1822;
Pred. No. 1.26e+00;
17; Mismatches 15; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NDV-1995 (Rel. 32, Created)
01-NDV-1995 (Rel. 32, Last sequence update)
01-NDV-1995 (Rel. 32, Last annotation update)
POTALITE MITCHONDRIAL PEPTIDE CHAIN RELEASE PACTDR PRECURSDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1300 IGLGVSPCLLLTALTTSNAAD-GMSLERFETIGDSFLKFATTDYLYHTLLD 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | |:: |||| | : |::: ||:|: : : : || :: : ||:
1 MGSGLPLVLLLTLLGSSHGTGPGWTLQ-L-KLKESFLTNSSYESSFLELLE 49
                                                                                                                                                                                                                                                                                                                    NATURE 368:32-38(1994).
-!- SIMILARITY: WITH OTHER ATP DEPENDENT HELICASES.
-!- SIMILARITY: CONTAINS A RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPAC2F7.17.
Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomycetes; Archiascomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 RNASE III DOMAIN.
208291 MW; 4F8E56BE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
DECH BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; 54489; 54489.
WORNPEP; K1244.8; CEO0273.
PROSITE; PS00517; RIBONUCLEASE_III; 1.
PFAM; PF000270; DEAD; 1.
PFAM; PF00270; DEAD; 1.
PFAM; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L14331; AAA28101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arity 31.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
148
1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 14
1554 182
1822 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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Bacteria; Pr
Raemophilus.
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                                                                                                                  T 8
RSEB_HAEIN
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Q10356;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swias Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                         1 ? MITOCHONDRION (POTENTIAL).
? 396 PUTATIVE MITOCHONDRIAL PEPTIDE CHAIN
RELEASE FACTOR.
396 AA, 44954 MM; 988689CB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJINE, 55020526.
GRUNDY F.J., WATERS D.A., TAKOVA T.Y., HENKIN T.M.;
"Identification of genes involved in utilization of acetate and
                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
Score 87; DB 1; Length 396;
Pred. No. 1.69e+00;
                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 86; DB 1; Length 272;
Pred. No. 2.27e+00;
12; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 30.1 KD PROTEIN IN ACUC 5'REGION (ORFA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
E89FDF9C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transport; Transmembrane
                                                                                                                                                                                                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMB1, 117309; AAA68282.1; --
EMB1, AF008220; AAC00300.1; --
EMB1, 299119; CAB14951.1; --
PIR, S39641; S39641.
SUBTILIST; BG10365; YTXD.
PROSITE; PS01307; MOTA; 1.
Hypothetical protein; Transport; '
TRANSMEM 9 29 POTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acetoin in Bacillus subtilis.";
Mol. Microbiol. 10:259-271(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 29 POI
38 58 POI
154 174 POI
188 208 POI
209 272 RM; 1
                                                                                                                                                                                                                                     281 LTHIPTGITVSMQDSRSQHQ 300
                                                                                                                                                                                                                                                        | |:|:| :|:: :||||:
54 LLHLPSGTSVTLHHARSQHH 73
                                                                                                                                                                 / Match 15.6%;
Local Similarity 45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 34.6%;
Matches 18; Conservative
                                                                                                                                                                                                    9: Conservative
                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                     396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          YTXD_BACSU
                                                                                                                            SEQUENCE
                                                                                                                                                               Query Match
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                                                                                                                                                                                                  Matches
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SEQUENCE FROM N.A.
STRAIN-ED, KRADO;
MEDLINE; 95350630.
MEDLINE; 95350630.
MEDLINE; 95350630.
MEDLINE; 95350630.
MEDLINE; 95350630.
MERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERYY B.A., MERRICK J.M., MCRENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCANNE J.D., SHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., WEIDBAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., OTTERBACK T.R., HANNA M.C., NGUTEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRWANN J.L., GEOGRAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SWALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
SIGMA-E FACTOR REGULATORY PROTEIN RSEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 269:496-512(1995).

-!- FUNCTION: SEEMS TO MODULATE THE ACTIVITY OF RPOE (SIGMA-E)
(BY SIMILARITY).

-!- SUBCELLULAR LOCATION: PERIPLASMIC (POTENTIAL).

-!- SIMILARITY: TO E.COLI RSEB AND P.AERUGINOSA MUCB.
164 IGTLVGLVLMLKNLNDPHMLGPNMAIALLTTLYGSLLANMVFNPIAAKLEEK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria; gamma subdivision; Pasteurellaceae;
                                     "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
SIGMA-E FACTOR REGULATORY PROTEIN RSEB HOMOLOG PRECURSOR.
RSEB OR HI0630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Mismatches 11; Indels
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01-077-1996 (Rel. 34, Last sequence update)
115-071-1998 (Rel. 36, Last annotation update)
HYPOTHEICAL 21.1 KD PROTEIN C22E12.03C IN CHROMOSOME I.
SPACZ2E12.03C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi: Ascomycota; Archiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SGLPLVILLTLIGSSHGTGPGNTLQLKIKESFLTNSSYESSFLE 46
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15.2%; Score 85; DB 1; L.
Best Local Similarity 29.5%; Pred. No. 3.04e+00;
Matches 13; Conservative 18; Mismatches 11
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SEQUENCE 315 AA; 35906 MW; 80BICIID CRC32;
                                                                                                                                                                                           315 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 191 AA.
                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32746; AAC22290.1; -.
TIGR; H10630; -.
                                                                                                                                                                                        STANDARD;
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24 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenzae Rd."
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01-NOV-1995 (
01-NOV-1995 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 POTENTIAL.
65 S->C: ALMOST NO CHANGE IN ACTIVITY.
65 S->A: NO CHANGE IN ACTIVITY.
66 D->N: UNABLE TO EXTRUDE TETRACYCLINE.
66 D->N: WORENTE RESISTANCE TO
TETRACYCLINE.
257 H->E: NO H+ TRANSLOCATION.
257 H->E: NO H+ TRANSLOCATION.
251 G->E: (IN REF. 2).
330 V->D (IN REF. 2).
330 Q->E: (IN REF. 2).
334 A->T (IN REF. 2).
354 A->T (IN REF. 2).
355 A->T (IN REF. 2).
356 A->T (IN REF. 2).
357 A->T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLIAE 974.26617.
BLATINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
EFFLUX, THIS IS AN ENERGY-DEPENDENT PROCESS THAT DECREASES THE ACCUMULATION OF THE ANTIBIOTIC IN WHOLE CELLS. THIS PROTEIN SUNCTIONS AS A METAL-TETRACKLINE/H ANTIPORTER. SUBCELLUINE: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE. SIMILARITY: BELONGS TO THE MAJOR FALILLIATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
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YGCS_ECOLI STANDARD;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHEFICAL METABOLITE TRANSPORT PROTEIN IN CYSJ-ENO INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                    PIR; A03507; YIECTO.

SOOSIE; PO00216; SUGAR_TRANSPORT_1; UNKNOWN_1.

Antiblotic resistance; Transmembrane; Inner membrane; Transport; Symport; Transposable element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%; Score 83; DB 1; Length 401; 31.0%; Pred. No. 5.43e+00; ative 13; Mismatches 23; Indels
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Conservative
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257 22
281 2
301 3
330 3
354 3
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ses 18; Conser
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Matches
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                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioincramatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                       DEVLIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGUYEN T.T., POSTLE K., BERTRAND K.P.; "Sequence homology between the tetracycline-resistance determinants of Inl0 and pBR322.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 90368755.

**AMASAKA T., NOUMI T., SAWAI T.;

**AMACHAIA... ONO N., AKASAKA T., NOUMI T., SAWAI T.;

**AMACHAIA... ONO N., AKASAKA T., NOUMI T., SAWAI T.;

**MACHAIA... ONO N., AKASAKA T., NOUMI T., SAWAI T.;

**Incharyoline transport...

**Incharyoline transport...

**J. Biol. Chem. 265:15525-15530(1990).

**J. Biol. Chem. 265:15525-15530(1990).

**J. BIOL. CHEM... AFTHACYCLINE BY AN ACTIVE TETRACYCLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAWAGUCHI A., ADACHI K., AKASAKA T., ONO N., SAWAI T.; "Metal-tetracycline/H+ antiporter of Escherichia coli encoded by transposon Inl0. Histidine 257 plays an essential role in H+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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15-DEC-1998 (Rel. 37, Last annotation update)
TETRACYCLINE RESISTANCE PROTEIN, CLASS B (TETA(B)) (METAL-
                                                                                                                                                                                                                                                                                                                                                  Score 84; DB 1; Length 191;
Pred. No. 4.07e+00;
11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      148 PVVLEENLI-TSQGPGTAMLFGLKLLEQVASKDKYNAVYKSL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                    EMBL; 270043; CAA93890.1; -.
Hypothetical protein.
SEQUENCE 191 AA; 21078 MW; D47EB47B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TETRACYCLINE/H+ ANTIPORTER).
                                                                                                                                                                                                                                                                                                                                                      Query Match 15.1%;
Best Local Similarity 33.3%;
Matches 14; Conservative
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MUTAGENESIS OF HIS-257.
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                          Schizosaccharomyces
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SEQUENCE FROM N.A.
MEDLINE; 83143319.
                                                         SEQUENCE FROM N.A.
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P02980;
                                                                         STRAIN-972;
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                                                             GANGLIOSIDES, GIXCOPROTEINS, AND GLYCOSAMINOGLYCAR.

-1- CAPRLYIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
-1- SUBCELLULAR LOCATION: LYSOSOMAL.
-1- SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES.
                 Blochem. Biophys. Res. Commun. 178:158-164(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL
D-ASFARIATE RECEPTOR SUBTYPE 2C) (NNDAR2C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 647;
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Aydrollsse; Glycosldae; Lysosome; Signal; Glycoprotein.
SignAL 1 24
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PROTON DONOR (POTENTIAL).
NUCLEOPHILE (POTENTIAL).
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1-> R (IN REF. 2).
15BCF158 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LPLVLLLTLLGSSHGT-G-PGMTLQLKL-KESFLTNS 38
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POTENTIAL.
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/; AAA37292.1; JOINED.

/; AAA37292.1; JOINED.

18; AAA37292.1; JOINED.

09; AAA37292.1; JOINED.
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Best Local Similarity 37.8%;
Matches 14; Conservative
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647
269
27
248
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647 AA;
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NME3_HUMAN
Q14957;
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ACT_SITE
CARBOHYD
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CONFLICT
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SEQUENCE
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                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most purposfit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedisb-sib.ch).
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GREGOR J., DAVIS N.W., KIRKPAIRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y., "The complete sequence of Escherichia coll K-12."; science 277:1453-1474(1997).
-1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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"Molecular cloning of mouse acid beta-galactosidase CDNA: sequence, expression of catalytic activity and comparison with the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P23780;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1997 (Rel. 20, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport; Transmembrane; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutherla; Rodentla; Sclurognathl; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-DBA/23;
MEDINE: 9128981.
NAMEA E., SUZUKI K.;
"Organization of the mouse acid beta-galactosidase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 5.43e+00;
Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 83; DB 1; Length 445;
                                                                                                                                          -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 GALLGLVLTH-LLAHRKFLLGSFLLLAATLVVMACLPSGSSLTL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMTLQLKLKESFLTNSSYE-SSFLELLEKLCLLLHPPSGTSVTL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blochem. Blophys. Res. Commun. 173:141-148(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                         ECOGENE; EG13126, YGCS.
PROSITE; PSO0216; SUGAR_TRANSPORT_1; FALSE_NEG.
PROSITE; PSO0217; SUGAR_TRANSPORT_2; 1.
PFAM; PF00083; sugar_tr; 1.
Hypothetical protein; Transport; Transmembrane; TRANSMEM
23 43 POTENTIAL.
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BDD078EF CRC32;
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EMBL; AE000360; AAC75813.1; ALT_INIT.
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Local Similarity 38.6%;
Nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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1135
1195
1274
3307
332
332
421
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GLB1 OR GLB-1 OR BGL.
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445 AA;
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TISSUE-BRAIN;
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CHAIN
TISOLE PRAIR;

MEDLINE; 97189248.

LIN Y.J., BOVETTO S., CARVER J.M., GIORDANO T.;

"CLOINING of the cDNA for the human NADA receptor NR2C subunit and its a "CLOINING of the cDNA for the human NADA receptor nad periphery.";

Brain Res. Mol. Brain Res. 43:57-64(1996).

1. Brain Res. Mol. Brain Res. 43:57-64(1996).

2. INTROLION: NADA RECEPTOR SUBTYPE DO GLUTAMATE-GATED ION CHANNELS POSSESES HIGH CALCIUM PERMANABILITY AND VOLTAGE-DEPENDENT SENSITIVITY TO MAGNESIUM AND IS MEDIATED BY GLYCINE.

2. SUBUNIT: HETERODIMER OF AN EPSILON SUBUNIT MAD A ZETA SUBUNIT.

3. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

4. TISSUE SPECIFICITY: MAININ IN BRAIN WITH PREDOMINANT EXPRESSION IS IN THE CREBELLUM, ALSO PRESENT IN THE HIPPOCAMPICS, AMYCDALA, CAUDATE NUCLEUS, CORPUS CALLOSUM, SUBTHALAMIC NUCLEI AND THALAMUS.

C. IN THE CERBELLUM, ALSO PRESENT IN THE HIPPOCAMPICS, AMYCDALA, CAUDATE NUCLEUS AND PANCREAS.

CAUDATE NUCLEUS, CORPUS CALLOSUM, SUBTHALAMIC NUCLEI AND THALAMUS.

C. IN THE HEART, SERLETAL MUSCLE AND PANCREAS.
                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of BaloinGormatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEGO_HUMAN STANDARD; PRT; 169 AA.
0295643.
15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38, Last annotation update)
(CII-3) (SUCCINARTE DEHYDROGENASE CYTOCHROME B560 SUBUNIT PRECURSOR (QPS1)
SUBCCINTAINE DEHYDROGENASE COMPLEX SUBUNIT C).
                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00060; 11g_chan; 1.
Receptor; Signal; Transmembrane; Postsynaptic membrane; Calcium;
Ionic channel; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. GLUTAMATE [NMDA] RECEPTOR SUBUNIT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
        Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Mammalia,
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (POTENTIAL).
FUNCTIONAL DETERMINANT OF NMDA
RECEPTORS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. No. 5.43e+00;
Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     671F9981 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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Pred. No. 5
13; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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MIM; 138254; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1233 AA; 134239
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Best Local Similarity 33.34;
Matches 20; Conservative
sapiens (Human)
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CARBOHYD
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SITE
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                                                                                                                                                                                                       MEDLINE; 99194224.

HERWARKE H., TANURA A., KOJIMA S., KITA K.;

#CYCOCITCME D in human complex II (succinate-ubiquinone oxidoreductase): cDNA cloning of the components in liver mitochondria and chromosomal assignment of the genes for the large (SDHC) and small (SDHD) subunits to 1421 and 11423.";

Cytogenet. Cell Genet. 79:132-138(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of the human SDHC gene encoding one of the integral membrane proteins of succinate-quinone oxidoreductase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 213:133-14(11998).

-1- FUNCTION: MONO-HEME CYTOCHROME B. MAY ACT AS A MEDIATOR OF LOW POTENTIAL COUPLES IN A BLECTRON FLOW THROUGH CARDIAC COMPLEX II. POTENTIAL COUPLES IN AN ELECTRON FLOW THROUGH CARDIAC COMPLEX II. SI INVOLED IN SYSTEM II OF THE MITOCHONDRIAL ELECTRON TRANSPORT CHAIN WHICH IS RESPONSIBLE FOR TRANSFERRING ELECTRONS FROM SUCCINATE TO UBIQUINONE (COENZYME Q).

-1- SUBJUNT: FORMS PART OF COMPLEX II CONTAINING FOUR SUBJUNTS: A 70 KD FLAVOPROTEIN (FP), A 27 KD IRON-SULFUR PROTEIN (IP), AND TWO OTHER MEMBRANE-ANCHORING PROTEINS, OPSI (CII-3) AND OPS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MITOCHONDRION (BY SIMILARITY).
SUCCINATE DEHYDROGENASE CYTOCHROME B560
SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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AU H.C., RAVAL P.J., SCHEFFLER I.E.; an integral membrane protein "The cDNA sequence of human CII-3, an integral membrane protein subunit of complex II of the mitochondria electron transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
Έ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 82; DB 1; Length 169;
Pred. No. 7.22e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 13; Indels
                                                                                                              Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i - SIMILARITY: BELONGS TO THE CYTOCHROME B560 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18610 MW; 3F37EF06 CRC32
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HEME (PROBABLE).
HEME (PROBABLE).
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EMBL, AF039589, AAC27993.1;
EMBL, AF039590, AAC27993.1;
EMBL, AF039591; AAC27933.1;
EMBL, AF039592; AAC27993.1;
GMBL, AF039592; AAC27993.1;
JOINED.
MIM; 602413;
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28.0%;
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127
168
71
127
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127
169 AA;
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                                                                                                                                                                          SEQUENCE FROM N.A.
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62 SLPMAMSICHRGTGIALSAGVSL-FGMS-ALLLPGNFES-YLELVKSLCL 108

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[1] SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LODGE J.M., AMIN I.I., DOUCE G.R., BROWN N.L., STEPHEN J.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: INVOLVED IN THE TRIGGERING OF INTRACELLULAR EVENTS THAT
LEAD TO MICKOBIAL INTENALIZATION OF THE INTESTINAL EPITHELION,
THESE EVENTS INCLUDE INCREASE IN CALCIOM LEVEL, REDISTRIBUTION OF
ACTIN MICROFILAMENTS, AND CHANGES IN THE NORMAL STRUCTURE OF THE
                                                                                                                                                                                                         Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KANIGA K., BOSSIO J.C., GALAN J.E.;
"The Salmonella typhimurium invasion genes invF and invG encode homologues of the AraC and PulD family of proteins.";
Mol. Microbiol. 13:555-568(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MICROVILLI.
SIMILARITY: TO YERSINIA OUTER MEMBRANE PROTEIN YOPN (LCRE).
                                                                                                                                                                                                                                                                                                                             GINOCCHIO C., PACE J., GALAN J.E.;
"Identification and molecular characterization of a Salmonella
"Identification and molecular characterization of a Salmonella
typhimurium gene involved in triggering the internalization of
salmonellae into cultured epithelial cells.";
Proc. Natl. Acad. Sci. U.S.A. 89:5976-5980(1992).
Score 82; DB 1; Length 372;
Pred. No. 7.22e+00;
17; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AA; 42436 MW; A345002E CRC32;
                                                                                                                01-07N-1994 (Rel. 29, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1996 (Rel. 33, Last sequence update)
INVASION PROFEIN INVE.
                                                                                      372 AA
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M90714; -; NOT_ANNOTATED_CDS.
EMBL; 098280; AAA441.1; -
EMBL; X75302; CAA53050.2; -
STYGENE; SG10187; INVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 26.1%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-69 FROM N.A.
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SEQUENCE OF 1-5 FROM N.A.
STRAIN=TML;
                                                                                    STANDARD;
                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
STRAIN-SR11 / SL1344;
MEDLINE; 92335220.
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MEDLINE; 95089692
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INVE_SALTY
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Release 3.1A John F. Collins, Blocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Mon Mar 20 12:31:44 2000; MasPar time 14.52 Seconds 372.517 Million cell updates/sec Tabular output not generated MPsrch_pp Run on:

1 MGSGLPLVLLLTLLGSSHGT.....SGTSVTLHHARSQHHVVCNT >US-09-092-296-15 (1-78) from US09092296.pep 558 Description: Perfect Score: Sequence:

PAM 150 Gap 11

Scoring table:

225878 seqs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb112

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_plage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 38.987; Variance 81.279; scale 0.480

Statistics:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8.06e-02 9.09e-01 1.22e+00 1.22e+00 1.22e+00 2.92e+00 3.89e+00 5.17e+00 5.17e+00 6.86e+00 6.86e+00 9.08e+00 9.08e+00 1.20e+01 1.20e+01 1.20e+01 1.20e+01 Pred. No. PROTEIN EXPORT MEMBRAN SBF PROTEIN PRECURSOR. APOCYTOCHROME B (EC. 1. RESTRICTION ENDONUCLEA. TRANSCRIPTION CO-REPRE FILLORES P PROTEIN. CYTOCHROME B (FRAGMENT HERRESVIRGS TYPE 6 DNA SBF PROTEIN. RHODDPIN. DIHYDROOROTASE. PUTATIVE TYROSINE KINA HYPOTHETICAL 56.7 KD P W08DZ.3 PROTEIN. CYTOCHROME B (FRAGMENT CYTOCHROME B (FRAGMENT CHALCONE SYNTHASE HOWO PURINERGIC P2Y11 RECEP Description 067102 0920J6 0920J6 068567 068567 P89688 099657 009582 0920J7 014968 003294 003295 501 2 382 11 382 11 863 14 11275 13 873 12 873 13 874 12 562 4 562 4 562 4 562 4 562 4 562 4 562 4 562 4 562 4 562 4 562 4 562 4 562 4 562 4 562 4 562 4 562 6 563 10 395 10 395 10 395 10 395 10 395 10 395 10 395 10 Query Match Length DB 118.1 116.7 Score Result

1.20e+01	1.20e+01	1.20e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	1.58e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e + 01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	2.08e+01	
TRANSCRIPTION FACTOR I	AMINOPEPTIDASE.	AMINOPEPTIDASE.	BCL-2 HOMOLOG.	CYTOCHROME B (FRAGMENT	CYTOCHROME B (FRAGMENT	NADH DEHYDROGENASE SUB	HYPOTHETICAL 43.3 KD P	CYTOCHRDME B.	CYTOCHRDME B.	POTASSIUM-TRANSPORTING	T25E12.11 PROTEIN.	N-METHYL-D-ASPARTATE R	INTEGRAL MEMBRANE PROT	INVASION PROTEIN.	ENT-KAURENE SYNTHASE.	PAIRED AMPHIPATHIC HEL									
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12	22	23	24	25	36	22	78	600	30	31	32	33	3.4	. 60	3.6	3.2	. cc	30	40	4.1	42	43	44	45	

ALIGNMENTS

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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-VF5;
BECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RELDMAN D.E., VORBEEER R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., DLSON G.J., SWANSON R.V.;
The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-VF5;
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SHEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
SUBMILTED (JUL.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AROOVIL6; AACA7060.1; -
SEQUENCE 501 AA, 55459 MW; E67F690C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                              01-AGG-1998 (TERMELAEL: 07, Created)
01-AGG-1998 (TERMELAEL: 07, Last sequence update)
01-AVV-1998 (TERMELAEL: 08, Last annotation update)
PROFEIN EXPORT MEMBRANE PROTEIN SECD.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Aquificales; Aquificaceae; Aquifex
                                          501 AA
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 392;353-358(1998).
                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                               Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
RESULT 1
10 067102;
057102;
07 01-AUG-1)
DT 01-AUG-1)
DE PROTEIN |
08 AQUIfex |
09 AQUIfex |
00 Batteria |
01 Batteria |
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Created) Last seguence update) 303 AA PRT; RESULT 2 PRELIMINARY;
ID Q220J6 PRELIMINARY;
AC Q220J6;
DT 01-MAY-1999 (TrEMBLE-1 10, DT 01-MAY-1999 (TrEMBLE-1 10, DT 01-MAY-1999) ò

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AVERY R.J.; * Isolation of a highly cytopathic lentivirus from a nondomestic cat."; J. Virol. 69:7371-7374(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=FIV-OMA;
MEDLINE; 96013855.
BARR M.C., ZOU L., HOLZSCHU D.L., PHILLIPS L., SCOTT F.W., CASEY J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                626 LGLTLALVTATTAGLIGTTTGTSA-LAVSLKLKEVMLQQSQINBATLGMLKILQRRLKQA 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 GDDVSHYLLYRVLGVAQEEGRLIDVYQN·KGRPLYK·-YAGSFLEAATKLCFKEAFPDSA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonas campestris.
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 92; DB 14; Length 863;
Pred. No. 1.22e+00;
16; Mismatches 27; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.5%; Score 92; DB 2; Length 209; Best Local Similarity 28.2%; Pred. No. 1.22e+00; Matches 20; Conservative 21; Mismatches 27; Indels
                                                                                                                                                                                                           STRAIN-BADRII;
ZHAMG B.-H., WILSON G.G.;
SUDMICTED (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; APG51092; AAC08983.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BARR M.C., ZOU L., LONG F., HOOSE W.A., AVERY R.J.;
Provinal organization and sequence analysis of feline
immunodeficiency virus isolated from a Pallas' cat.";
Virology 228:84-91(1997):
Wheby 156928; AAB49325.1; -.
Polyprotein
SEQUENCE 863 AA, 99281 MW; 6928E60F CRC32;
               01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
RESTRICTION ENDONUCLEASE R.XBAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TEMBLrel. 03, Created)
01-MAY-1997 (TEMBLrel. 03, Last sequence update)
01-MOY-1998 (TEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feline immunodeficiency virus.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                   209 AA; 23834 MW; 1EC63D0B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           863 AA; 99281 MW; 6928E60F CRC32;
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Best Local Similarity 33.3%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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62 SVTLHHARSQH 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 SLRLPNTQGQR 98
                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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MEDLINE; 97177285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                       Kanthomonas.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 5
P89688
P89688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
ID Q9W6S7
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Mitochondrion.
Eukaryota; Fungi; Chytridiomycota; Chytridiomycetes; Blastocladiales;
Blastocladiaceae; Allomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINE; 96226032.
PAQUIN B., LANG B.F.;
The mitochondrial DNA of Allomyces macrogynus: the complete genomic sequence from an ancestral fungus.";
J., Mol. Biol. 255:688-701(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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01-NOV-1996 (TEMBLE1. 01, Casted)
01-NOV-1998 (TEMBLE1. 01, Last sequence update)
01-NOV-1998 (TEMBLE1. 08, Last annotation update)
APOCYTOCHROME B (EC 1.10.2.2) (UBIQUINOL.-CYTOCHROME C REDUCTASE)
(CYTOCHROME BCI COMPLEX).
                                                                                                                                                            SEQUENCE FROM N.A.
BOETTNER M., LAAFF M., SUTER-CRAZZOLARA C.;
Identification of a novel member of the TGFDeta superfamily.",
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ011969; CAA09891.1; -
EMBL; AJ011970; CAA09891.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 POMILQLK-LKESFL-INSSYESSFLELLERLCLILHLPSGTSVTLHHARS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 16.7%; Score 93; DB 11; Length 303; Local Similarity 36.7%; Pred. No. 9.09e-01; es 18; Conservative 11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 LFLLLLLLLLSWPSQGDALALPEQRRSLSESQLNPDELRGREQDLLSRL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LPLVLLLTLLG-SSHGTGFGMTLQLK-LKESFLTNSSYESSFLELLEKL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.7%; Score 93; DB 8; Length 382; 33.3%; Pred. No. 9.09e-01; Pathye 15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SBF PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4 ID 068567 PRELIMINARY; PRT; 209 AA. AC 068567 OC 98567, DT 01-AUG-1998 (TrEMBLrel. 07, Created) DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                SIĞNAL 1 33 POTENTIAL.
SEQUENCE 303 AA; 33438 MW; 01C35FCC CRC32;
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PFAM; PP00032; cytcchrome_b_c; 1.
PFAM; PF00033; cytcchrome_b_n; 0.
Oxldoreductase; Mitochondrion.
SEQUENCE 382 AA; 43467 MW; A21E1AB1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 33.3%;
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Q37395
Q37395;
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Gaps

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SEQUENCE FROM N.A.
SHAFER H.B., METLIAN P., MCKNIGHT M.L.;
Syst, Biol. 0:0-0(0).
-1- CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = Q + 2
FERROCYTOCHROME C.
-1- COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
EMBL; 081355, AAB57646.1; -.
EMBL; 08032; GYLCCHOME—D.N; 1.
PFAM; PP00033; GYLCCHOME—D.N; 1.
Mitochondrion; Electron transport; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDDLINE: 94181269.
THONDSON J. ROSENTHAL L.J.;
FRENKEL N., ROSENTHAL L.J.;
A transforming fragment within the direct repeat region of human herpestvirus type 6 that transactivates HIV-1.";
Concogene 9:1167-2175(1994).
EMBL; X73675; CAA52028.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 GLTIVHLLFLYETGSNNPTGLNSNMD-KIPPHPYFSYKDVF-GLILMLAILLNL 216
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Testudines;
Cryptodira; Trionychoidea; Carettochelyidae; Carettochelys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GLPLVLLITLIGSSHGTGPGNTIQIALKESFLTNSSYESSFLELLERLCLLLHL 57
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092007;
01-MAY-1999 (TREMBLrel. 10, Created)
01-MAY-1999 (TREMBLrel. 10, Last sequence update)
01-MAY-1999 (TREMBLrel. 12, Last annotation update)
SPF PROTEIN PRECURSOR.
SPF OR GDF15.
MUS musculus (Mouse).
Mus musculus (Mouse).
Elkaryota; Metaca; Chordata; Craniata; Vertebrata; Mammalla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 15.8%; Score 88; DB 8; Length 297; Local Similarity 31.5%; Pred. No. 3.89e+00; Local Similarity 10; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
15.6%; Score 87; DB 14; Length 143
Best Local Similarity 47.2%; Pred. No. 5.17e+00;
Matches 17; Conservative 4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human herpesvirus 6.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.7 9 PRELIMINARY; PRT; 143 AA. 2659582 PRELIMINARY; PRT; 143 AA. 2659582 Ol-NoV-1996 (TrEMBLrel. 01, Created) Ol-NoV-1996 (TrEMBLrel. 01, Last sequence update) HERPESVIRUS TYPE 6 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75; CAA52028.1; -.
143 AA; 13317 MW; 597857A6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 1
297 297
297 AA; 33587 MW; 7D5808B5 CRC32;
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STRAIN-129SVJ;
BOETTNER M., LAAFF M., SUIER-CRAZZOLARA C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Betaherpesvirinae; Roseolovirus.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
VERMARA D., WADE P.A., JONES P.L., SHI Y.-B., WOLFFE A.P.;
VERMARA D., WADE P.A., JONES P.L., SHI Y.-B., WOLFFE A.P.;
FUNCTIONAL analysis of the SIN3-histone deacetylase: RFD3-Rbap48-histone H4 connection in the Xenopus cocyte.";
Submitted (NAX-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, RF154112; AAD34644.1;
SEQUENCE 1275 AA: 145088 MW; EB1942F4 CRC32;
                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 97105885.
HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 28.9%; Pred. No. 2.92e+00;
Matches 11; Conservative 15; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 16.5%; Score 92; DB 13; Length 127 Local Similarity 27.5%; Pred. No. 1.22e+00; Local 11; Conservative 15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-M129;
HIMMELREICH R., HILBERT H., LI B.-C.;
SUBMILTEG (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AE000042; AAB96079.1; -
SEDUENCE 879 AA; 101086 MW; 94D217E0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 8
003305
003305
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003305
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAY-1999 (TrEMBLrel. 04, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CYTOCHROME B (FRAGMENT).
CARCHICCHELYS insculpta (pitted-shelled turtle).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TIEMBLED. 02, Created)
01-FEB-1997 (TIEMBLED. 02, Last sequence update)
01-NOV-1998 (TIEMBLED. 08, Last annotation update)
F11_ORF879 PROTEIN.
Mycoplasma pneumoniae.
              Q9W6S7;
01-NOV-1999 (TLEMBLrel. 12, Last sequence update)
01-NOV-1999 (TLEMBLrel. 12, Last sequence update)
01-NOV-1999 (TLEMBLrel. 12, Last annotation update)
TRANSCRIPTION CO-REPRESSOR SIN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      935 VLGLKRDKNDSAAIQLRLKEPMDIEAEDYNPAFLDMVRNL 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| : ::||:||: : ::||:1|| : 13 ILGSSHGTGPGMTLQLKLKESF-LTNSSYESSFLELLEKL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             677 EGIPKDSNY-SSFVHLLDQKSLFLQLAKVSGIDINENK 713
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Nucleic Acids Res. 24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-M129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HERRMANN R.;
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PRELIMINARY;
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67 H-ARSQHHVVCNT 78
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SEQUENCE
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003295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE, 92250505.
KUNZ D., GERARD N.P., GERARD C.;
The human leukocyte platelet activating factor receptor. cDNA
cloning, cell surface expression, and construction of a novel epitope-
                                                   HSIAO E.C., KONTARIS L.G., ZIMMERS T.A., SEBALD S.M., SITZMANN J.V., HBIVNH T.V., LEE S.-J.;
"Growth/differentiation factor-15: a new TGF-beta family member induced following liver and bile duct injury.", EMBL, AND1967: CA069890.1;
EMBL, AND1967: CA069890.1;
EMBL, AND1968: CA069890.1;
EMBL, AND1968: CAA08890.1;
EMBL, AND1968: CAA08890.1;
EMBL, AND1968: CAA08890.1;
EMBL, AND1968: AND41410.1;
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86; DB 4; Length 322;
Pred. No. 6.86e+00;
13; Mismatches 22; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 ALVLLIFLLSSLGNCAVMGVIVKHRQLRTVTNAFILS-LSLSDLLTALLCLPAA 148
"Identification of a novel member of the TGFbeta superfamily.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 PLVLLILITIGSSHGTGFGWTLQIALKESFLTNSSYESSFLELLEKICLILIHIPSG 60
                                                                                                                                                                                                                                                                    ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                    Score 87; DB 11; Length 303;
Pred. No. 5.17e+00;
10; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                         20 LFLLLLLLLLSWPSQGDALAMPEQRRSGPESQLNADELRGRFQDLLSRL 68
                                                                                                                                                                                                                                                                                                         5 LPLVLLITLIG-SSHGTGPGWTLQLKL-KESFLTNGSYESSFLELLEKL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEVINBURNE J., AINSCOUGH R.; SUBDMitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TEMBLIA: 01, Created)
01-NOV-1996 (TEMBLIA: 01, Last sequence update)
01-NOV-1998 (TEMBLIA: 08, Last annotation update)
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Last annotation update)
                                                                                                                                                                            Signal.
SIGNAL 1 29 POTENTIAL.
SEQUENCE 303 AA; 33256 MW; FBBF45FE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 AA; 33096 MW; 70F54EC8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                           PRT; 322 AA.
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01-NOV-1996 (TIEMBLREL 01, Last seq.
01-JAN-1999 (TIEMBLREL 09, Last annow WOBD2.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bearing analog.";
J. Biol. Chem. 267:9101-9106(1992).
BEDL: M76676; AAB97766.1;
PFAM: PF00001; 7tm_1: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                    Match 15.6%;
Local Similarity 36.7%;
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 34.5%;
Matches 19; Conservative
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                                                                                                                                                                  HSSP; P18075; 1BMP
                                     SEQUENCE FROM N.A.
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014968
014968;
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Q23220
Q23220,
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Matches
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ESCUENCE FROM N.A.
REDLINE; 94150718
RA WILSON R., ANDERSON K., BAXNES C., BERKS M.,
RA WILSON R., AINSCOUGH R., ANDERSON K., BAXNES C., BERKS M.,
RA BONETELD J., EDRYON J., CONNELL M., COPERT J., COOPER J., COLLSON A.,
RA GRANDR A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
ANDES M., KERSHAM J., KIRSTEN J., LATREILE P.,
ADMES M., MERSHAM J., KIRSTEN J., LATREILE P.,
RA LIGHTNING J., LLOYD C., MCHMERAY A., MORTIMORE B., O'CALLAGHAN M.,
RA LIGHTNING J., PERCY C., RIFKEN L., SONNHARMER E., STADEN N., SULSTON J.,
SWALDON N., SNITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THERRY-MIEG J., THOMAS K., VANDIN M., VANGHAN K., WATERTON J.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RY "2.2 MD Of CONTIQUOUS NUCLECTIME SEQUENCE from Chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Testudines;
Cryptodira; Testudinoidea; Emydidae; Trachemys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GLPLVLLTLLGSSHGTGPGWTLQLKLKESFLINSYESSFLELLEKLCLLLHL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 15.4%; Score 86; DB 5; Length 562; Best Local Similarity 31.5%; Pred. No. 6.86e+00; Matches 23; Conservative 19; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 15.2%; Score 85; DB 8; Length 297; Best Local Similarity 33.3%; Pred. No. 9.08e+00; Matches 18; Conservative 9; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JVL-1999 (TrEMBLrel. 10, Last annotation update)
CYTOCHROME B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 270271; CAA94232.1; -.
SEQUENCE 562 AA; 63331 MW; 5272E400 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 297
297 AA; 33479 MW; IBCBCFAC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trachemys scripta (Red-eared slider turtle). Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
FEDERSPEL N.A., CONWAY A.R., DAVIS K., BRENDEL V.,
PALM C.J., AU M., ARADOR R., CHUNG E., KURTZ D.B., BUEHLER E.,
DEWAR K., FERG J., KIM C., LI Y., SHINN P., SUN H., OJI O.,
OSBORNE B., SHEN Y.K., TORIUMI M., VYOTSKAIA V., YU G., THEOLOGIS A.,
ECKER J., DAVIS R.W.;
SUDMITTED (FEB-1997) to the EMBL/Genbank/DDBJ databases.
EMBL; U89959, AAC24368.1; -.
EMBL; U89959, AAC24368.1; -.
EMBL; G89959, AAC44568.1; -.
EMBL; G89959, AAC4456.1; -.
EMBL; G89959, AAC4456.1; -.
ENGL; AAC4476.1; -.
ENGL; AAC4456.1; -.
ENGL; AAC446.1; -.
ENGL; AAC4476.1; -.
EN
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 AGLAIVHLLFLHETGSNNPTGLNSNAD-KIPFHPYFSYKD-LLGLILMLTLLLTLA 217
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                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Testudines;
Cryptodira; Testudinoidea; Bataguridae; Heosemys.
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Local Similarity 33.3%; Pred. No. 9.08e+00;
Les 14; Conservative 12; Mismatches 15; Indels
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Best Local Similarity 32.1%; Pred. No. 9.08e+00;
Matches 18; Conservative 11; Mismatches 25; Indels
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O 23674;

DT 01-JAN-1998 (TERBLrel. 05, Created)

DT 01-JAN-1998 (TERBLrel. 05, Last sequence update)

DT 01-JAN-1999 (TERBLrel. 05, Last sequence update)

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01-JUL-1997 (ITEMBLrel. 04, Last sequence update)
01-MAY-1999 (ITEMBLrel. 10, Last annotation update)
CYTOCHRONE B (FRAGMENT).
Heosemys spinosa.
Mitochondrion.
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297 AA; 33321 MW; AD3A6749 CRC32;
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